

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:33:27 ; Search time 100 Seconds

(without alignments)
13088.964 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268

Sequence: 1 cccaagagaccactctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	0.8	33	2	US-08-451-822A-9
2	33	0.8	33	4	US-08-323-430-9
3	33	0.8	33	1	US-08-471-570-15
4	30	0.7	30	1	US-07-947-663-15
5	30	0.7	30	1	US-08-400-323-18
6	25.8	0.6	30	1	US-07-997-133-4
7	25.8	0.6	30	5	US-07-997-133-4
8	25	0.6	25	2	US-08-859-998-431
9	25	0.6	25	2	US-08-859-998-431
10	25	0.6	25	4	US-09-225-928-431
11	25	0.6	25	4	US-09-225-928-431
12	25	0.6	25	4	US-08-451-822A-10
13	25	0.6	25	4	US-08-323-430-10
14	24	0.6	24	1	US-08-371-001-4
15	24	0.6	24	2	US-08-451-822A-11
16	24	0.6	24	2	US-08-323-430-11
17	24	0.6	24	5	PCT-US96-00331-4
18	23.4	0.5	40	4	US-09-306-290-33
19	22.6	0.5	50	1	US-08-420-443-1
20	22.4	0.5	28	1	US-07-631-717A-5
21	22.4	0.5	28	1	US-08-166-717D-5
22	22	0.5	22	5	PCT-US96-00331-5
23	22	0.5	22	5	PCT-US96-00331-5
24	22	0.5	30	1	US-08-471-570-18
25	22	0.5	45	1	US-08-522-623-6
26	22	0.5	45	1	US-08-522-623-6
27	22	0.5	45	5	PCT-US93-03256-6

28	22	0.5	45	5	PCT-US93-03256-11	Sequence 11, Appl
29	21.8	0.5	37	4	US-09-526-542-19	Sequence 19, Appl
30	21.8	0.5	40	4	US-09-306-290-34	Sequence 34, Appl
31	21.8	0.5	43	2	US-08-686-599A-14	Sequence 14, Appl
32	21.8	0.5	44	1	US-08-686-596B-9	Sequence 9, Appl
33	21.8	0.5	44	4	US-09-142-334-13	Sequence 13, Appl
34	21.4	0.5	25	2	US-08-678-039A-4	Sequence 4, Appl
35	21.2	0.5	38	4	US-09-454-704A-7	Sequence 7, Appl
36	21.2	0.5	42	3	US-08-757-024-16	Sequence 16, Appl
37	21.2	0.5	43	3	US-08-757-024-15	Sequence 15, Appl
38	21.2	0.5	44	3	US-08-757-024-14	Sequence 14, Appl
39	21.2	0.5	45	2	US-08-471-025-44	Sequence 44, Appl
40	21.2	0.5	46	3	US-08-757-024-13	Sequence 13, Appl
41	21.2	0.5	46	3	US-08-757-024-12	Sequence 12, Appl
42	21.2	0.5	47	3	US-08-757-024-11	Sequence 11, Appl
43	21.2	0.5	48	3	US-08-757-024-10	Sequence 10, Appl
44	21.2	0.5	49	3	US-08-757-024-9	Sequence 9, Appl
45	21.2	0.5	50	3	US-08-757-024-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-451-822A-9/c
Sequence 9, Application US/08451822A
Patent No. 5863888

GENERAL INFORMATION:

APPLICANT: Dionne, Craig A

APPLICANT: Crumley, Greg

APPLICANT: Jaye, Michael C

APPLICANT: Schlessinger, Joseph

TITLE OF INVENTION: Fibroblast Growth Factor Receptors

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Legal Department

STREET: 500 Arcoia Road

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08451,822A

FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/323,430

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,372

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/549,587

FILING DATE: 06-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: A0496E

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3816

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-451-822A-9

Query Match 0.8%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 TATCCACACATTAACGGCAGTGTAAACATGA 2739

DB 33 TATCCACACATTAACGGCAGTGTAAACATGA 1

RESULT 2

US-08-323-430-9/c

; Sequence 9, Application US/08323430
; Patent No. 6344546

; GENERAL INFORMATION:

; APPLICANT: Dionne, Craig A

; APPLICANT: Crumley, Greg

; APPLICANT: Jaye, Michael C

; APPLICANT: Schlessinger, Joseph

; TITLE OF INVENTION: Fibroblast Growth Factor Receptors

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Legal Department

; STREET: 500 Arcoia Road

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/323,430

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US to be assigned

; FILING DATE: 21-AUG-1992

; APPLICATION NUMBER: US 07/549,587

; FILING DATE: 06-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Goodman, Rosanne

; REGISTRATION NUMBER: 32,534

; REFERENCE/DOCKET NUMBER: A0496

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 454-3817

; TELEFAX: (215) 454-3808

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; US-08-323-430-9

; Query Match

; Best Local Similarity 100.0%; Pred. No. 26;

; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; RESULT 3

; US-08-471-570-15/c

; Sequence 15, Application US/08471570

; Patent No. 5750371

; GENERAL INFORMATION:

; APPLICANT: IGARASHI, Koichi

; APPLICANT: SENOO, Masaharu

; APPLICANT: WATANABE, Tatsuya

; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,570

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/149,664

; FILING DATE:

; APPLICATION NUMBER: US 07/743369

; FILING DATE: 16-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: LINEK, Ernest V

; REGISTRATION NUMBER: 29822

; REFERENCE/DOCKET NUMBER: 40897

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; TELEX: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid, synthetic DNA

; US-08-471-570-15

; Query Match

; Best Local Similarity 84.6%; Pred. No. 28;

; Matches 33; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

; RESULT 4

; US-07-947-683-15/c

; Sequence 15, Application US/07947683

; Patent No. 5589451

; GENERAL INFORMATION:

; APPLICANT: WILSON, STEVEN E.

; TITLE OF INVENTION: METHODS AND TREATMENTS FOR

; TITLE OF INVENTION: CORNEAL HEALING WITH HEPATOCYTE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P. O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,683
FILING DATE: SEPTEMBER 21, 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:311/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-947-683-15

Query Match 0.7%: Score 30; DB 1; Length 30;
Best Local Similarity 100.0%: Pred. No. 1.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 GATTGAGTTCCTATATTCGGAATGTAC 1271
DB 30 GATTGAGTTCCTATATTCGGAATGTAC 1

RESULT 5
US-08-400-323-18/c
Sequence 18, Application US/08400323
Patent No. 5703047
GENERAL INFORMATION:
APPLICANT: Wilson, Steven E.
TITLE OF INVENTION: Methods and Treatments for Corneal
TITLE OF INVENTION: Healing with Growth Factors
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,323
FILING DATE: 09-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:431/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-400-323-18

Query Match 0.7%: Score 30; DB 1; Length 30;

Best Local Similarity 100.0%: Pred. No. 1.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1242 GATTGAGTTCCTATATTCGGAATGTAC 1271
DB 30 GATTGAGTTCCTATATTCGGAATGTAC 1

RESULT 6
US-07-997-133-4/c
Sequence 4, Application US/07997133
Patent No. 5288855
GENERAL INFORMATION:
APPLICANT: Bergonzoni, Laura
APPLICANT: Mazue, Guy
APPLICANT: Isacchi, Antonella
APPLICANT: Roncucci, Romeo
APPLICANT: Sarmentos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P. C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/997,133
FILING DATE: 28-DEC-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,755
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288855man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-226-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-997-133-4

Query Match 0.6%: Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%: Pred. No. 1.5e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2488 TGTGGCATGCAGTGCCTCCAGAGACC 2516
DB 30 TGTGGCATGCAGTGCCTCCAGAGACC 2

RESULT 7
US-07-997-133-4/c
Sequence 4, Application US/07997133
GENERAL INFORMATION:
APPLICANT: Bergonzoni, Laura
APPLICANT: Mazue, Guy
APPLICANT: Isacchi, Antonella

```

:
: APPLICANT: Roncucci, Romeo
: APPLICANT: Sarmiento, Paolo
: TITLE OF INVENTION: Extracellular Form of the Human
: TITLE OF INVENTION: Fibroblast Growth Factor Receptor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESSES:
: ADDRESSSEE: P.C. C. SPYAK, MCCLELLAND, MAIER & NEUSTADT,
: STREET: 1755 Jefferson Davis Highway, Fourth Floor
: CITY: Arlington
: STATE: Virginia
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/997,133
: FILING DATE: 28-DEC-1992
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/642,755
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Oblon, Norman F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 769-226-0
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)521-4500
: TELEFAX: (703)486-2347
: TELEFAX: 248855 OPAT UR
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-07-997-133-4

Query Match 0.6%; Score 25.8; DB 5; Length 30;
Best Local Similarity 93.1%; Pred. No. 1.5e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2488 TGTGGCATGCAGTGCCTCCAGAGACC 2516
DB 30 TGTGGCATGCAGTGCCTCCAGAGACC 2

RESULT 8
: US-08-859-998-431
: Sequence 431, Application US/08859998
: Patent No. 5994076
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: APPLICANT: Jekhadze, George
: TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
: TITLE OF INVENTION: EXPRESSION
: NUMBER OF SEQUENCES: 1375
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: Fish & Richardson, P.C.
: STREET: 2200 Sand Hill Road, Suite 100
: CITY: Menlo Park
: STATE: CA
: COUNTRY: US
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: INFORMATION FOR SEQ ID NO: 432:
: SEQUENCE CHARACTERISTICS:

```

```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/859,998
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Field, Bret E.
: REGISTRATION NUMBER: 37,620
: REFERENCE/DOCKET NUMBER: 09096/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-322-5070
: TELEFAX: 415-854-0875
: INFORMATION FOR SEQ ID NO: 431:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: OTHER INFORMATION: oligonucleotide primer
: US-08-859-998-431

Query Match 0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 GCTCCATGCTGTGCTGGCGCCAC 792
DB 1 GCTCCATGCTGTGCTGGCGCCAC 25

RESULT 9
: US-08-859-998-432/C
: Sequence 432, Application US/08859998
: Patent No. 5994076
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Jekhadze, George
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
: TITLE OF INVENTION: EXPRESSION
: NUMBER OF SEQUENCES: 1375
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: Fish & Richardson, P.C.
: STREET: 2200 Sand Hill Road, Suite 100
: CITY: Menlo Park
: STATE: CA
: COUNTRY: US
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/859,998
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Field, Bret E.
: REGISTRATION NUMBER: 37,620
: REFERENCE/DOCKET NUMBER: 09096/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-322-5070
: TELEFAX: 415-854-0875
: INFORMATION FOR SEQ ID NO: 432:
: SEQUENCE CHARACTERISTICS:

```


LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-432

Query Match 0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GCCCAGCGGCTGCCCTACTCAAG 1203
Db 25 GCCCAGCGGCTGCCCTACTCAAG 1

RESULT 10
US-09-225-928-431
Sequence 431, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 431:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 431:
US-09-225-928-431

Query Match 0.6%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 GCTCCATGCTGTGCTGGCGCCAC 792
|||||

Db 1 GCTCCATGCTGTGCTGGCGCCAC 25

RESULT 11
US-09-225-928-432/C
Sequence 432, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 432:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 432:
US-09-225-928-432

Query Match 0.6%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GCCCAGCGGCTGCCCTACTCAAG 1203
Db 25 GCCCAGCGGCTGCCCTACTCAAG 1

RESULT 12
US-08-451-822A-10
Sequence 10, Application US/08451822A
Patent No. 5863888
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPPLICANT: Grumley, Greg
APPPLICANT: Jaye, Michael C
APPPLICANT: Schlesinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-451-822A-10

Query Match 0.6%; Score 25; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 ACCATGTCAGCTGGGCGCTTCA 295
Db 21 ACCATGTCAGCTGGGCGCTTCA 45

RESULT 13
US-08-323-430-10
Sequence 10, Application US/08323430
Patent No. 6344546
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPLICANT: Cronley, Greg
APPLICANT: Jaje, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/323,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0496
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-323-430-10

Query Match 0.6%; Score 25; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 ACCATGTCAGCTGGGCGCTTCA 295
Db 21 ACCATGTCAGCTGGGCGCTTCA 45

RESULT 14
US-08-371-001-4
Sequence 4, Application US/08371001
Patent No. 5783683
GENERAL INFORMATION:
APPLICANT: Morrison Ph.D., Richard
TITLE OF INVENTION: Methods and Composition for Treating
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich
STREET: 401 "B" Street, Suite 1700
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,001
FILING DATE: January 10, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Broctman, Harris F.
REGISTRATION NUMBER: 35,461
REFERENCE/DOCKET NUMBER: P00095050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-3630
TELEFAX: (619) 236-1048
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid
US-08-371-001-4

Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 AAGTGTGCAGATGGATTACGTC 230
|||||
Db 1 AAGTGTGCAGATGGATTACGTC 24

RESULT 15

US-08-451-822A-11/C
; Sequence 11, Application US/08451822A
; Patent No. 5863888
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451.822A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,430
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,372
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-451-822A-11

Query Match 0.6%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 503 TGCACCTGGGGCCCAACATAGGA 526
|||||
Db 24 TGCACCTGGGGCCCAACATAGGA 1

Search completed: December 11, 2002, 17:47:48
Job time : 105 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:31:32 : Search time 551 seconds
(without alignments)
17443.791 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 cccaaggagccactcttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table:
IDENTITY-MNC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	32	0.7	32	13	AAQ23618		3'mbek - a bek pro
C	2	30	0.7	30	18	AAAT63287		Probe for amplifie
C	3	30	0.7	30	19	AAV05503		Probe for RGF rece
C	4	26.2	0.6	50	22	AAI29297		Human SNP oligonuc
C	5	25.8	0.6	30	12	AAO13309		Probe OAB984 for b
C	6	25	0.6	25	24	ABK6343		Human gene specifl
C	7	25	0.6	25	24	ABK6344		Human gene specifl
C	8	25	0.6	42	20	AAK84630		Oligomer used in D
C	9	25	0.6	45	13	AAQ23619		Bek4a - a PCR prim

C	10	24.8	0.6	49	22	AAI29254	Human SNP oligonuc
C	11	24.6	0.6	31	22	AAI30470	Human single nucle
C	12	24.6	0.6	50	21	AAA98316	Human MSH6 fragmen
C	13	24.4	0.6	42	16	AAAT05796	D101 linked oligon
C	14	24.2	0.6	47	20	AAK52549	Human genome biail
C	15	24.2	0.6	47	21	AAZ66994	Human map-related
C	16	24	0.6	24	13	AAO23620	Bek1B - a PCR prime
C	17	24	0.6	24	17	AAAT31054	Human fibroblast g
C	18	24	0.6	45	22	AAI28218	Human SNP oligonuc
C	19	23.6	0.6	31	22	AAAF58621	Murine c-kit exon
C	20	23.6	0.6	47	21	AAA64611	AU rich sequence 1
C	21	23.6	0.6	50	24	ABNT5039	Human ac1 wt cMNR
C	22	23.6	0.6	49	22	AAI28400	Human SNP oligonuc
C	23	23.6	0.6	50	22	AAI28400	Human SNP oligonuc
C	24	23.6	0.6	50	22	AAI75629	Human SNP oligonuc
C	25	23.4	0.5	40	22	AAH20352	Human SNP oligonuc
C	26	23.4	0.5	46	24	AAK59735	HHV6 virus p41 gen
C	27	23.4	0.5	47	23	AAH88384	Altele discriminat
C	28	23	0.5	31	22	AAI30469	CNS disorder-relat
C	29	23	0.5	44	22	AAI30410	Human SNP oligonuc
C	30	22.8	0.5	44	22	AAI30581	Human SNP oligonuc
C	31	22.6	0.5	41	22	AAK84629	Oligomer used in D
C	32	22.6	0.5	41	22	AAI31923	Human SNP oligonuc
C	33	22.6	0.5	46	22	AAI28459	Human SNP oligonuc
C	34	22.6	0.5	47	20	AAK52599	Human genome biail
C	35	22.6	0.5	48	8	AAAT71061	5'-3' probe for ex
C	36	22.6	0.5	49	19	AAVA1447	Nucleotide sequenc
C	37	22.6	0.5	49	22	AAE98419	Human cDNA clone B
C	38	22.6	0.5	50	15	AAO66922	Poly-da 50mer prob
C	39	22.6	0.5	50	22	AAAF60897	Conjugate forming
C	40	22.6	0.5	50	23	AAK58336	CDNA #1012 encodin
C	41	22.4	0.5	50	24	ABN89414	Polymorphism detec
C	42	22.4	0.5	28	19	AAV44045	Mouse bFGF recepto
C	43	22.4	0.5	42	22	AAI31043	Human SNP oligonuc
C	44	22.4	0.5	46	24	AAK59731	Altele discriminat
C	45	22.2	0.5	47	21	AAZ69037	Human map-related
C	46	22.2	0.5	50	22	AAI29199	Human SNP oligonuc

ALIGNMENTS

RESULT 1
AAQ23618/c
ID AAQ23618 standard; DNA; 32 Bp.

XX AC AAQ23618;
XX DT 21-MAY-1992 (first entry)
XX DE 3'mbek - a bek probe.
XX KW Bacterially expressed kinase; CFS-1;
XX KW PGDF; tyrosine kinase; ss.
XX OS Synthetic.
XX PN WO9200999-A.
XX PD 23-JAN-1992.
XX PF 03-JUL-1991; 91WO-US04745.
XX PR 06-JUL-1990; 90US-0549587.
XX PA (RORE) RORER INT HOLDINGS.
XX PI Dione CA, Crumley G, Jaye MC, Schlessinger J;
XX DR WPI: 1992-056827/07.
XX DR P-PSDB; AAR20750.
XX PT New fibroblast growth factor receptor proteins - useful in
PT treating gf-mediated conditions e.g. angiogenesis of tumours,

PT mitogenic effects in psoriasis, arthritis
 XX Disclosure: Page 25; 65pp; English.
 XX The oligonucleotide 3'mbek was used to screen a one day old human
 CC brain stem library as it is complementary to the 3' end of the partial
 CC murine bek coding sequence (Kornbluth et al., Mol. Cell Biol. 8:
 CC 5541-5544, 1988). The fragment obtd. was amplified by Bek4A (AAQ23619)
 CC and Bek1B (AAQ23620) primers, and the obtd. full length bek clone was
 CC sub- sequently sequenced and the protein sequence deduced. Receptor
 CC proteins encoded by this cDNA sequence may be used in pharmaceutical
 CC compans. to inhibit undesirable heparin-binding growth factor mediated
 CC cellular responses or to inhibit the binding of an opportunistic pathogen
 CC to human cells. Such undesirable responses may be growth factor
 CC stimulated angiogenesis and vascularisation of tumours, mitogenic effects
 CC in psoriasis, arthritis, atherosclerosis and benign prostatic
 CC hypertrophy. The derived bek protein may also be used for screening
 CC drugs. See also AAQ21003,4 and AAQ23610-7.
 XX
 SQ Sequence 32 BP; 6 A; 5 C; 7 G; 14 T; 0 other;
 Query Match 0.7%; Score 32; DB 13; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2708 ATCCACACATTAACGCGACTTTAAACATGA 2739
 DB 32 ATCCACACATTAACGCGACTTTAAACATGA 1
 RESULT 2
 AAT63287/C
 ID AAT63287 standard; DNA: 30 BP.
 XX AAT63287;
 AC AAT63287;
 XX 21-MAY-1997 (first entry)
 DT
 XX
 XX Probe for amplified fragment of FGF receptor gene.
 DE
 XX
 XX Cornea: proliferation; in vivo; hepatocyte growth factor; injury; PCR;
 KW keratinocyte growth factor; ocular surgery; epithelium; endothelium;
 KW expression; receptor; polymerase chain reaction; amplification; primer;
 KW healing; beta-actin; upstream; downstream; intron; ss.
 XX
 OS Synthetic.
 XX
 XX US5589451-A.
 PN
 XX
 PD 31-DEC-1996.
 XX
 XX 21-SEP-1992; 92US-0947683.
 PF
 XX 21-SEP-1992; 92US-0947683.
 PR
 XX 21-SEP-1992; 92US-0947683.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Wilson SE;
 PI
 XX
 DR WPI: 1997-076878/07.
 XX
 PT Promoting or suppressing corneal cell proliferation - using
 PT hepatocyte growth factor or calcium ions resp., e.g. for treating
 PT corneal injury or for preserving corneal tissue prior to
 PT transplantation
 XX
 XX Example 1; Column 11-12; 25pp; English.
 PS
 CC The invention relates to methods for promoting corneal cell
 CC proliferation in vivo by treating the cells with hepatocyte growth factor
 CC (HGF) and optionally keratinocyte growth factor (KGF). Methods for
 CC suppressing corneal cell growth include administering Ca ions to the
 CC cells. The methods are used for the treatment of corneal tissue injury

CC following accidental injury, ocular surgery or due to corneal disorders
 CC caused by abnormal healing processes of the corneal epithelium and
 CC endothelium. The methods are based on the discovery that corneal tissue
 CC can express mRNA for HGF, KGF and their respective receptors. The
 CC discovery was shown by PCR amplification using the primers AAT63273-87.
 CC This probe is used to detect the 205 bp fragment amplified from the
 CC fibroblast growth factor (FGF) receptor 2 cDNA by primers AAT63283 and
 CC AAT63286. The probe corresponds to nucleotides 30-59 of the FGF receptor
 CC 2 gene.
 XX
 SQ Sequence 30 BP; 11 A; 7 C; 4 G; 8 T; 0 other;
 Query Match 0.7%; Score 30; DB 18; Length 30;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1242 GATGAGGTTCTCTATATTCGATGTAC 1271
 DB 30 GATGAGGTTCTCTATATTCGATGTAC 1
 RESULT 3
 AAV05503/C
 ID AAV05503 standard; DNA: 30 BP.
 XX AAV05503;
 AC AAV05503;
 XX
 XX 01-MAY-1998 (first entry)
 DT
 XX
 XX Probe for FGF receptor DNA.
 DE
 XX
 XX Inhibition; corneal epithelial cell; differentiation; treatment;
 KW hepatocyte growth factor; HGF; keratinocyte growth factor; KGF;
 KW dry eye; keratoconjunctivitis sicca; probe; receptor;
 KW fibroblast growth factor; FGF; ss.
 KW
 OS Synthetic.
 XX
 OS Homo sapiens.
 XX
 XX US5703047-A.
 PN
 XX
 PD 30-DEC-1997.
 XX
 XX 09-MAR-1995; 95US-0400323.
 PF
 XX 09-MAR-1995; 95US-0400323.
 PR
 XX 21-SEP-1992; 92US-0947683.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Wilson SE;
 PI
 XX
 DR WPI: 1998-076459/07.
 XX
 PT Inhibition of corneal cell differentiation - by using hepatocyte
 PT growth factor and/or keratinocyte growth factor
 XX
 XX Example 1; Columns 17-18; 36pp; English.
 PS
 CC The present sequence was used in the development of a novel method
 CC for the inhibition of corneal epithelial cell differentiation. The
 CC method comprises contacting the cells with a hepatocyte growth
 CC factor (HGF) and/or keratinocyte growth factor (KGF). When HGF and
 CC KGF are both used, the cells can be contacted with them
 CC sequentially or simultaneously. The HGF and/or KGF is in a timed
 CC release delivery system, especially comprising biodegradable
 CC polymer microcapsules. The HGF and/or KGF are administered
 CC topically. The method is used for treating dry eye, especially
 CC keratoconjunctivitis sicca.
 XX
 SQ Sequence 30 BP; 11 A; 7 C; 4 G; 8 T; 0 other;
 Query Match 0.7%; Score 30; DB 19; Length 30;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1242 GATTGAGTCTCTATATTCGAGATGAAC 1271
Db 30 GATTGAGTCTCTATATTCGAGATGAAC 1

RESULT 4
ID AAL29297 standard; DNA; 50 BP.
XX AAL29297;
AC AAL29297;
DT 24-JAN-2002 (first entry)
DE Human SNP oligonucleotide #2505.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyloid; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN W0200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CUBA-) CUBAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
XX
PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2100; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 7 A; 17 C; 14 G; 12 T; 0 other;

Query Match 0.6%; Score 26.2; DB 22; Length 50;
Best Local Similarity 79.5%; Pred. No. 1e+04;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 323 CCTGTGCTCCGCGCCGCTCTCTAGTTAGTTAGG 361
Db 11 CCTGTGCTCCGCGCCGCTCTCTAGTTAGTTAGG 49

RESULT 5
ID AAQ13309/C
XX AAQ13309 standard; DNA; 30 BP.
XX
AC AAQ13309;
XX
DT 28-OCT-1991 (first entry)
XX
DE Probe OAB984 for bFGF receptor DNA.
XX
KW Basic fibroblast growth factor; human; ss.
XX
OS Synthetic.
XX
PN W09111459-A.
XX
PD 08-AUG-1991.
XX
PF 21-JAN-1991; 91WO-EP00103.
XX
PR 23-JAN-1990; 90GB-0001466.
XX
PA (FARM) FARMITALIA C ERBA SRL.
XX
PI Bergonzoni L, Mazue G, Isacchi A, Roncucci R, Sarmientos P;
XX
DR WPI; 1991-252611/34.
XX
PT Extracellular form of human fibroblast growth factor receptor -
XX
PT used to treat tumours, abnormal angiogenesis e.g. diabetic
XX
PT retinopathy, rheumatoid arthritis and arteriosclerosis and as
XX
XX
PS Example 1; Page 11; 29pp; English.
XX
CC The probe was used to screen a human placental lambda gt11 cDNA
CC library for the gene encoding basic FGF receptor. It was designed
CC from the partial cDNA clone published by Ruta et al, 1988.
XX
SQ Sequence 30 BP; 5 A; 8 C; 11 G; 6 T; 0 other;

Query Match 0.6%; Score 25.8; DB 12; Length 30;
Best Local Similarity 93.1%; Pred. No. 9.6e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2488 TGTGTGGCATGCAAGTCCCTCCAGAGACC 2516
Db 30 TGTGTGGCATGCAAGTCCCTCCAGAGACC 2

RESULT 6
ID ABR66343 standard; DNA; 25 BP.
XX ABR66343;
AC ABR66343;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #431.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS Homo sapiens.
XX
PN US6352829-B1.
XX
PD 05-MAR-2002.

```

PF 05-JAN-1999; 99US-0225928.
XX 21-MAY-1997; 97US-0859998.
PR (CLON-) CLONTECH LAB INC.
PA Chenchik A, Jakhadze G, Bibilashvili R;
PI WPI: 2002-314699/35.
DR
XX Producing sub-population of labeled nucleic acids, useful for analysing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers
XX
PS Example 3: SEQ ID NO 431; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where
CC each gene specific primer has a sequence complementary to a distinct
CC rRNA, and each labeled NA is generated using a single gene specific
CC primer. The method is useful for producing a sub-population of labeled
CC NAs which is useful for analysing the differences in the RNA profiles
CC between several different physiological sources, where the method
CC comprises producing subpopulation of labeled NAs for each physiological
CC source to identify differences in the populations, where the comparison
CC is preferably performed by hybridising the labeled NAs for each of the
CC distinct physiological sources to an array of probe NAs stably
CC associated with the surface of a substrate to produce a hybridisation
CC pattern for each of the sources, and comparing the patterns for each of
CC the sources, where differential gene expression assays are
CC utilised in differential expression analysis of diseased a normal
CC tissue e.g. neoplastic a normal tissue, or different tissue or
CC subcellular types. The present sequence is a human gene specific PCR
CC primer used in the method of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from USPTO at
CC http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.
XX
SO Sequence 25 BP; 3 A; 10 C; 7 G; 5 T; 0 other:
Query Match 0.6%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. NO. 1.4e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 768 GCTCCATGCTGTGCGCCGCCAANC 792
DB 1 GCTCCATGCTGTGCGCCGCCAANC 25
RESULT 7
ABK66344/c
XX ABK66344 standard; DNA; 25 BP.
XX AC ABK66344;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #432.
XX KW Primer: ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN U56352829-B1.
XX PD 05-MAR-2002.
XX 05-JAN-1999; 99US-0225928.

```

XX	21-MAY-1997:	97US-0859998.
PR	(CLON-)	CLONTECH LAB INC.
XX	Chenclik A,	Jokhadze G, Bibilashvili R;
PA	WPI: 2002-314699/35.	
PI		
XX		
DR		
XX		
PT	Producing sub-population of labeled nucleic acids, useful for analysing	
PT	differences in RNA profiles between several different physiological	
PT	sources, using set of distinct gene specific primers.	
PS	Example 3: SEQ ID NO 432; 11pp: English.	
XX		
CC	The invention relates to producing a sub-population of labeled nucleic	
CC	acids (NAs) comprising contacting a NA sample from a physiological	
CC	source, with a pool of 50 distinct gene specific primers under suitable	
CC	conditions to enzymatically generate sub-population of NAs, where	
CC	each gene specific primer has a sequence complementary to a distinct	
CC	mRNA, and each labeled NA is generated using a single gene specific	
CC	primer. The method is useful for producing a sub-population of labeled	
CC	NAs which is useful for analysing the differences in the RNA profiles	
CC	between several different physiological sources, where the method	
CC	comprises producing subpopulation of labeled NAs for the different	
CC	physiological sources, comprising the populations for each physiological	
CC	source to identify differences in the population, where the comparison	
CC	is preferably performed by hybridising the labeled NAs for each of the	
CC	distinct physiological sources to an array of probe NAs stably	
CC	associated with the surface of a substrate to produce a hybridisation	
CC	pattern for each of the sources, and comparing the patterns for each of	
CC	the sources, where differential gene expression assays are	
CC	utilised in differential expression analysis of diseased tissue or	
CC	tissue e.g. neoplastic a normal tissue, or different tissue or	
CC	subtissue types. The present sequence is a human gene specific PCR	
CC	primer used in the method of the invention.	
CC	Note: The sequence data for this patent did not form part	
CC	of the printed specification, but was obtained in electronic	
CC	format directly from USPRO at	
CC	http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.	
XX		
SQ	Sequence 25 BP; 3 A; 7 C; 11 G; 4 T; 0 other:	
	Query Match	0.6%; Score 25; DB 24; Length 25;
	Best Local Similarity	100.0%; Pred. No. 1.4e+04;
	Matches 25; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1179 GCCCGACGGGCTGCCCTCAAG 1203	
DB	25 GCCCGACGGGCTGCCCTCAAG 1	
RESULT 8		
AAxB4630		
ID	AAxB4630 standard: DNA: 42 BP.	
XX		
AC	AAxB4630:	
DT	16-SEP-1999 (first entry)	
XX		
DE	Oligomer used in DNA obstruction assay.	
XX		
KW	DNA obstruction assay; receptor interaction; ligand interaction;	
KW	biological sample characterisation; diagnosis; diabetes; heart disease;	
KW	infectious disease; inflammatory disease; neoplastic disorder;	
KW	autoimmune disease; central nervous system disorder; ss.	
XX		
OS	Synthetic.	
XX		
XX	WO9931267-A1.	
PN		
PD	24-JUN-1999.	
XX		

PF 18-DEC-1998: 98WO-US26894.
 XX
 PR 18-DEC-1997: 97US-0068035.
 XX
 PA (SEPR-) SEPRACOR INC.
 XX
 PI Gao Y, Heefner DL, Jones SW, Zepp CM;
 DR WPI: 1999-405040/34.
 XX
 PT Simultaneous identification of novel biological targets
 XX
 PS Example 2: Page 53; 125pp; English.
 XX
 CC This sequence represents an oligonucleotide used to test a DNA
 CC obstruction assay for assessing interaction between receptors and
 CC ligands. The invention relates to a method for the characterisation of
 CC biological samples, and comprises detecting the binding of individual
 CC members of a library of molecular probes to molecular components in the
 CC sample. The method comprises: (a) contacting the sample with a library of
 CC molecular probes to allow them to bind to their specific binding
 CC partners; and (b) detecting any binding of individual members of the
 CC library of molecular probes to molecular components in the sample using a
 CC homogeneous assay system, in which the binding pattern of members of the
 CC library with the sample provides a molecular fingerprint of the sample.
 CC The method can be used for characterising biological samples for
 CC molecular components such as proteins, glycoproteins, polynucleotides,
 CC polysaccharides, lipids, organic molecules or inorganic molecules. They
 CC can be used for diagnosing a disease or condition in a patient and for
 CC monitoring the efficacy of a drug or therapy in a patient. They can be
 CC used for conditions such as diabetes, infectious disease, inflammatory
 CC disease, heart disease, neoplastic disorders, autoimmune disease and
 CC central nervous system disorders.
 CC
 SQ Sequence 42 BP: 32 A; 2 C; 2 G; 6 T; 0 other;
 Query Match 0.6%; Score 25; DB 20; Length 42;
 Best Local Similarity 75.6%; Pred. No. 1.8e+04;
 Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 4224 AACACAGCAAAATTAATGTCACGCACTTAAAAA 4264
 DB 2 AAAAAAAAAAATATATAGATGCAATTAATAAAAAA 42
 RESULT 9
 AAQ23619
 ID AAQ23619 standard; DNA: 45 BP.
 XX
 AC AAQ23619;
 XX
 DT 21-MAY-1992 (first entry)
 XX
 DE Bek4A - a PCR primer.
 XX
 KW Bacterially expressed kinase; CFS-1; amplification;
 KW PGDF; tyrosine kinase; ss.
 XX
 OS Synthetic.
 XX
 FN WO9200999-A.
 XX
 PD 23-JAN-1992.
 XX
 PF 03-JUL-1991; 91WO-US04745.
 XX
 PR 06-JUL-1990; 90US-0549587.
 XX
 PA (RORE) RORER INT HOLDINGS.
 XX
 PI Dionne CA, Crumley G, Jaye MC, Schleesinger J;
 DR WPI: 1992-056827/07.

DR P-PSDB; AAR20750.
 XX
 PT New fibroblast growth factor receptor proteins - useful in
 PT treating gf-mediated conditions e.g. angiogenesis of tumours,
 PT mitogenic effects in psoriasis, arthritis
 XX
 PS Disclosure: Page 25; 65pp; English.
 XX
 CC The oligonucleotide 3'mek (AAQ23618) was used screen a one day old human
 CC brain stem library as it is complementary to the 3' end of the partial
 CC murine bek coding sequence (Kornbluth et al., Mol. Cell Biol. 8:
 CC 5541-5544 1988). The fragment obtd. was amplified by Bek4A and
 CC Bek1B (AAQ23620) primers, and the obtd. full length bek clone was sub-
 CC equently sequenced and the protein sequence deduced. Receptor proteins
 CC encoded by this cDNA sequence may be used in pharmaceutical compns. to
 CC inhibit undesirable heparin-binding growth factor mediated cellular
 CC responses or to inhibit the binding of an opportunistic pathogen to
 CC human cells. Such undesirable responses may be growth factor stimulated
 CC angiogenesis and vascularisation of tumours, mitogenic effects in
 CC psoriasis, arthritis, atherosclerosis and benign prostatic hypertrophy.
 CC The derived bek protein may also be used for screening drugs.
 CC See also AAQ21003.4 and AAQ23610-7.
 CC
 SQ Sequence 45 BP: 10 A; 11 C; 12 G; 12 T; 0 other;
 Query Match 0.6%; Score 25; DB 13; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 271 ACCATGTCAGCTGGGTCGTTTCA 295
 DB 21 ACCATGTCAGCTGGGTCGTTTCA 45
 RESULT 10
 AAL29254/C
 ID AAL29254 standard; DNA: 49 BP.
 XX
 AC AAL29254;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #2462.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 XX
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections.

```

XX PS Claim 1; Page 2088; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cyclochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 49 BP; 3 A; 3 C; 4 G; 39 T; 0 other:
XX
Query Match 0.6%; Score 24.8; DB 22; Length 49;
Best Local Similarity 72.7%; Pred. No. 2.2e+04;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
QY 4225 ACAGACAAATTAATGTCAGCACTTAATAAAAAAAAAAAAAA 4268
DB 49 AATATTAACATTAATGCGCCCAAAAAAAAAAAAAAAAAAAAAA 6
XX
RESULT 11
AAI30470
ID AAI30470 standard; DNA; 31 BP.
XX
AC AAI30470;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) FGF3 2.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,C)
FT /tag=a
FT /standard_name="single nucleotide polymorphism"
XX
XX WO200166800-A2.
XX
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
XX
XX 07-MAR-2000; 2000US-0187510.
XX
XX 22-MAY-2000; 2000US-0206129.
XX
XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI; 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
XX sites, useful in methods for predicting the presence, absence or
XX severity of a particular phenotype or disorder (e.g. diabetes)
XX associated with a particular genotype -
XX
XX Claim 1; Page 87; 145pp; English.
XX

```

```

CC The invention relates to the identification of nucleic acid molecules
CC (AAI95313-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 other:
XX
Query Match 0.6%; Score 24.6; DB 22; Length 31;
Best Local Similarity 87.1%; Pred. No. 1.9e+04;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1034 ACCGGCCATCTCCAGCCGACTGCCGC 1064
DB 1 ACCGGCCATCTCCAGCCGCGCTGCCGC 31
XX
RESULT 12
AAI98316
ID AAI98316 standard; DNA; 50 BP.
XX
AC AAI98316;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human MSH6 fragment 8/exon 8 to 10 DNA Ref-Seq fragment #3.
XX
DE Human mismatch repair gene; hMSH6; disease predisposition; genotype;
KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
KW neoplastic disease; drug development; ds.
XX
OS Homo sapiens.
XX
FH DE19909878-A1.
XX
XX 07-SEP-2000.
XX
XX 06-MAR-1999; 99DE-1009878.
XX
XX 06-MAR-1999; 99DE-1009878.
XX
XX (UYDR) UNIV DRESDEN TECH.
XX
XX Plasmacke J, Kruppa C, Schackert H;
XX
XX WPI; 2000-588378/56.
XX
XX Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
XX determining predisposition to cancer and for development of drugs -
XX
XX Disclosure: Fig 3; 14pp; German.
XX
XX This invention describes a novel method of determining a predisposition
XX to disease by genotyping a subject's DNA sequence (A) of the human
XX mismatch repair gene, MSH6 at specified positions and comparing with
XX reference DNA sequences, optionally taking into account all possible
XX combinations of variations of the individual mutations, including any
XX chosen absolute number of variations. (A), and analysis of their
XX sequences, are useful for the following: (i) determining a predisposition
XX to disease, especially colorectal, endometrial and ovarian carcinoma and
XX leukemia; (ii) determining an increased mutation rate (frequency of base
XX substitutions, insertions and/or deletions) in eukaryotic cells; (iii)
XX predicting the progression, severity and survival time of patients with
XX neoplastic disease; (iv) the development of therapeutic and 'life-style'
XX drugs; (v) predicting individual differences in response to known
XX chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);
XX (vi) optimizing individual treatments and interventions against
XX neoplasia; (vii) controlling the mutation rate in eukaryotic cells, in
XX vitro or in vivo; (viii) constructing genes and vectors, particularly for
XX

```


Query Match 0.6%; Score 24.2; DB 20; Length 47;
 Best Local Similarity 78.4%; Pred. No. 3e+04;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3300 AGAGCTGGAATACTTTGCTTCAGCGAATAATCG 3336
 |||||
 DB 9 AGAGATGCAAAAACCTAGGCTTCTGGGTAAATCG 45

RESULT: 15

AAZ66994
 ID AAZ66994 standard; DNA; 47 BP.

AAZ66994;

10-SEP-2001 (first entry)

DE Human map-related diallelic marker SEQ ID NO:1341.

KW Human genome; diallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

Key Location/Qualifiers
 FT replacement(24,T)
 FT /*tag=2
 FT /standard_name="single nucleotide polymorphism"

PN WO954500-A2.

PD 28-OCT-1999.

PP 21-APR-1999; 99WO-1B00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

PA (GEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

DR MPI; 2000-013267/01.

PT Novel diallelic markers used to construct a high density disequilibrium
 map of the human genome -

PS Claim 1: Page 516; 2745pp; English.

CC AAZ65654 to AAZ69578 represent human diallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the diallelic markers. The diallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the sequence listing
 CC from the present invention.

SO Sequence 47 BP; 17 A; 6 C; 15 G; 9 T; 0 other;

Query Match 0.6%; Score 24.2; DB 21; Length 47;
 Best Local Similarity 78.4%; Pred. No. 3e+04;

Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3300 AGAGCTGGAATACTTTGCTTCAGCGAATAATCG 3336
 |||||
 DB 9 AGAGATGCAAAAACCTAGGCTTCTGGGTAAATCG 45

Search completed: December 11, 2002, 17:45:48
 Job time : 557 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:33:27 ; Search time 7153 seconds

(without alignments)
17364.850 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268

Sequence: 1 cccaaggaccactctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl :
1: gb_ba : *
2: gb_htg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vt : *
15: em_ba : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
28: em_un : *
29: em_vt : *
30: em_hum : *
31: em_inv : *
32: em_htg : *
33: em_htg : *
34: em_htg : *
35: em_htg : *
36: em_htg : *
37: em_htg : *
38: em_sy : *
39: em_hum : *
40: em_hum : *
41: em_hum : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4268	100.0	4268	6	AX332811	AX332811 Sequence
2	4268	100.0	4268	6	AX334117	AX334117 Sequence
3	4268	100.0	4268	6	AX336422	AX336422 Sequence
4	4268	100.0	4268	9	HUMKSAWI	M87770 Human fibro
5	3386	79.3	3415	9	HSGFRBE	X52832 Human dex m
6	3244	76.0	3248	9	HSGFRZUB	X52832 Human dex m
7	3244	76.0	3248	9	HSGFRZUB	X52832 Human dex m
8	3244	76.0	3248	9	HSGFRZUB	X52832 Human dex m
9	2781	65.2	3106	9	HUMKGFRA	X52832 Human dex m
10	2670	62.6	3244	6	AX329662	X52832 Human dex m
11	2670	62.6	3244	6	AX329662	X52832 Human dex m
12	2642	61.9	3809	4	AF211257	M87771 Human secre
13	2603	61.0	3080	9	HUMKGFRA	AF211257 Canis fam
14	2456	57.8	2466	6	AX481471	M97193 Homo sapien
15	2437	57.1	2481	9	HUMTK14	M55614 Human fibro
16	2404	56.3	2923	9	AB030077	AB030077 Homo sapi
17	2399	56.2	2826	9	AB030078	AB030078 Homo sapi
18	2399	56.2	3071	9	AB030075	AB030075 Homo sapi
19	2397	56.2	2868	9	AB030076	AB030076 Homo sapi
20	2397	56.2	2876	9	AB030074	AB030074 Homo sapi
21	2397	56.2	2941	9	AB030073	AB030073 Homo sapi
22	2310	54.1	3306	10	MUSBEKFGFA	M64441 M. musculus
23	2202	51.6	3120	10	MUSBEKFGFA	M64441 M. musculus
24	2191	51.3	2650	9	HSBRFR	X55441 Mouse bek g
25	2191	51.3	2676	6	AR007159	X55441 Mouse bek g
26	1977	46.3	2273	4	AF184968	AR007159 Sequence
27	1898	44.5	2711	4	BTGFRPCR	AF184968 Orcyolag
28	1896	44.4	3013	9	AK026508	Z68150 B. taurus mr
29	1857	43.5	3025	9	HUMKSAMAA	AK026508 Homo sapi
30	1828	42.8	2716	5	CHKECK3	M35718 Human hepar
31	1817	42.6	1954	6	AR007158	M35196 Chicken tyr
32	1728	40.5	3037	10	MUSKGFRA	AR007158 Sequence
33	1692	39.7	2310	6	AR007160	M63503 Mouse kerat
34	1687	39.5	2621	5	GCBEK	AR007160 Sequence
35	1661	38.9	94605	9	AF410480S2	X61992 G. gallus mr
36	1661	38.9	174398	9	AC009988	AF410480S2 Homo sapi
37	1661	38.9	174398	9	AC009988	AC009988 Homo sapi
38	1660	38.9	126467	9	AF487553	AC009988 Homo sapi
39	1579	37.0	2015	10	RPFIBGFB	AF487553 Homo sapi
40	1555	36.4	2117	10	RPFIBGFB	Z53139 R. rattus mr
41	1486	34.8	2967	5	PMGFR2	X74332 P. walli mr
42	1367	32.0	2675	5	PMGFR2	X74332 P. walli mr
43	1367	32.0	2675	5	PMGFR2	L19869 Notophthalm
44	1330	31.2	3104	5	XJGFR2	AR007135 Sequence
45	1318	30.9	1603	6	AR007157	X65943 X. laevis mr

ALIGNMENTS

RESULT 1
AX332811
LOCUS AX332811 4268 bp DNA
DEFINITION Sequence 3320 from Patent WO0194629.
ACCESSION AX332811
VERSION AX332811.1 GI:18123445
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature


```
OY 1981 GGCAACCTCCGGAATACCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCTATGAC 2040
| | | | |
DB 1981 GGCAACCTCCGGAATACCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCTATGAC 2040
OY 2041 ATTAACGCTGTTCCTGAGAGACAGATGACCTTCAAGAGCTTGGTGTCTATGACCTACCAG 2100
| | | | |
DB 2041 ATTAACGCTGTTCCTGAGAGACAGATGACCTTCAAGAGCTTGGTGTCTATGACCTACCAG 2100
OY 2101 CTGGCCAGAGGCATGAGTACTTGGCTTCCCAAAAATGATTTATTCGAGATTTCAGGCC 2160
| | | | |
DB 2101 CTGGCCAGAGGCATGAGTACTTGGCTTCCCAAAAATGATTTATTCGAGATTTCAGGCC 2160
OY 2161 AGAATGTTTGGTACGAGAAACAATGTGATGAATAATAGCAGACTTGGACCTGCCAGA 2220
| | | | |
DB 2161 AGAATGTTTGGTACGAGAAACAATGTGATGAATAATAGCAGACTTGGACCTGCCAGA 2220
OY 2221 GATATCAACATATAGATATGATTAACAAAAGCCAAATGGGCGCTTCCAGTCAAGTGG 2280
| | | | |
DB 2221 GATATCAACATATAGATATGATTAACAAAAGCCAAATGGGCGCTTCCAGTCAAGTGG 2280
OY 2281 ATGGCTCCAGAGCCCTGTTTGTATAGATATACATCATCATGAGTGTATGTCCTCTTC 2340
| | | | |
DB 2281 ATGGCTCCAGAGCCCTGTTTGTATAGATATACATCATCATGAGTGTATGTCCTCTTC 2340
OY 2341 GGGGTGTAATGTTGGGAGATCTTACCTTTAGGGGCTCGCCCTACCCAGGATTCCTGTC 2400
| | | | |
DB 2341 GGGGTGTAATGTTGGGAGATCTTACCTTTAGGGGCTCGCCCTACCCAGGATTCCTGTC 2400
OY 2401 GAGGAACCTTTTAAAGCTGTGAAGGAGACACAGATGTGATAGCCAGCACTGAC 2460
| | | | |
DB 2401 GAGGAACCTTTTAAAGCTGTGAAGGAGACACAGATGTGATAGCCAGCACTGAC 2460
OY 2461 AACGAACCTGTACATGATGATGAGGAGCTGTGGCATGACCTGCCCTCCAGAGCAACG 2520
| | | | |
DB 2461 AACGAACCTGTACATGATGATGAGGAGCTGTGGCATGACCTGCCCTCCAGAGCAACG 2520
OY 2521 TTCAGCAGTTGGTGAAGACTTGGATCGAATCTCCTCCTCAACCAATGAGGATAC 2580
| | | | |
DB 2521 TTCAGCAGTTGGTGAAGACTTGGATCGAATCTCCTCCTCAACCAATGAGGATAC 2580
OY 2581 TTGGACCTCAGCCAACTCTCGAAGATATTCACCTGATACCTGACACAAAGTTCT 2640
| | | | |
DB 2581 TTGGACCTCAGCCAACTCTCGAAGATATTCACCTGATACCTGACACAAAGTTCT 2640
OY 2641 TGTTCCTCAGAGATGATGTTGTTTTTTCAGAGCCCAATGCCCTTACGAACATGCTT 2700
| | | | |
DB 2641 TGTTCCTCAGAGATGATGTTGTTTTTTCAGAGCCCAATGCCCTTACGAACATGCTT 2700
OY 2701 CCTCAGTATCCACATAAACGCGAGTGTAAACATGATGATGATGCTGCTGCTGCC 2760
| | | | |
DB 2701 CCTCAGTATCCACATAAACGCGAGTGTAAACATGATGATGATGCTGCTGCTGCC 2760
OY 2761 CAACAGAGAGAGAGCTGGGAACCTACCTACCTAGCAGAGGAGAGACCATGCTCCAGAG 2820
| | | | |
DB 2761 CAACAGAGAGAGAGCTGGGAACCTACCTACCTAGCAGAGGAGAGACCATGCTCCAGAG 2820
OY 2821 TTGTTGCTCCACTTGTATATATGATGATGAGAGATTAATTAATGCAAAAGTATACGA 2880
| | | | |
DB 2821 TTGTTGCTCCACTTGTATATATGATGATGAGAGATTAATTAATGCAAAAGTATACGA 2880
OY 2881 TATGTATAAGATTTTATACAGTTGAACCTTGAATCTTCCCGAGAGAGAGAAAGTTT 2940
| | | | |
DB 2881 TATGTATAAGATTTTATACAGTTGAACCTTGAATCTTCCCGAGAGAGAGAAAGTTT 2940
OY 2941 TCTGGAGAGCTGAGCTGCCCAAGCCACCATGTAACCCCTTCACCTGCGCTGCTTCG 3000
| | | | |
DB 2941 TCTGGAGAGCTGAGCTGCCCAAGCCACCATGTAACCCCTTCACCTGCGCTGCTTCG 3000
OY 3001 GCTGTGAGACCTAGAGCTCAAGTGGAGCTGCTGCTTCTCTGTTATTTTGTAA 3060
| | | | |
DB 3001 GCTGTGAGACCTAGAGCTCAAGTGGAGCTGCTGCTTCTCTGTTATTTTGTAA 3060
OY 3061 TAATTGGAGAGATTTTATGTCAGACACACTTACAGAGCACAATAATGCACTATATAGTGC 3120
| | | | |

DB 3061 TAATTGGAGAGATTTTATGTCAGACACACTTACAGAGCACAATAATGCACTATAGTGC 3120
OY 3121 TGGATGATGTAATAATATATTCATTAATTAATATATATATATATATATATATATATAT 3180
| | | | |
DB 3121 TGGATGATGTAATAATATATTCATTAATTAATATATATATATATATATATATATATAT 3180
OY 3181 TATTTTGTATGATTTTAAATGATGTCCTCAATGACCTAGAAAAATGCTCTCTT 3240
| | | | |
DB 3181 TATTTTGTATGATTTTAAATGATGTCCTCAATGACCTAGAAAAATGCTCTCTT 3240
OY 3241 TTTTATAGCTATTTGCTTAATGCTGTTTACACATTAATTTCTTAAATTTTACCCAGCA 3300
| | | | |
DB 3241 TTTTATAGCTATTTGCTTAATGCTGTTTACACATTAATTTCTTAAATTTTACCCAGCA 3300
OY 3301 GAGTGGAAAAATACCTTTTCTTCAGGGAATGATATACCTTAATTAATTAAT 3360
| | | | |
DB 3301 GAGTGGAAAAATACCTTTTCTTCAGGGAATGATATACCTTAATTAATTAAT 3360
OY 3361 TGGTAATATCAAAACAATTAATATATATATATATATATATATATATATATATATAT 3420
| | | | |
DB 3361 TGGTAATATCAAAACAATTAATATATATATATATATATATATATATATATATATATAT 3420
OY 3421 ATCAGGACACAGCAGAGACTAATATATATATATATATATATATATATATATATATAT 3480
| | | | |
DB 3421 ATCAGGACACAGCAGAGACTAATATATATATATATATATATATATATATATATATAT 3480
OY 3481 TTTGAAAAAGAAATATTTACATATATATATATATATATATATATATATATATATAT 3540
| | | | |
DB 3481 TTTGAAAAAGAAATATTTACATATATATATATATATATATATATATATATATATAT 3540
OY 3541 TTTGTTTAAATGCTGTCAGAGATGTTCTTACCTCTCTTAAATGCTCATATTTAA 3600
| | | | |
DB 3541 TTTGTTTAAATGCTGTCAGAGATGTTCTTACCTCTCTTAAATGCTCATATTTAA 3600
OY 3601 AAGACTCATTCATAGGAAGTGTTCATTTTGTGTGCAACCTCTCATTAAGTGCCTTA 3660
| | | | |
DB 3601 AAGACTCATTCATAGGAAGTGTTCATTTTGTGTGCAACCTCTCATTAAGTGCCTTA 3660
OY 3661 CAACGCTAACGAGACTTCCCAAGATTAATGATGATGATGATGATGATGATGATGATG 3720
| | | | |
DB 3661 CAACGCTAACGAGACTTCCCAAGATTAATGATGATGATGATGATGATGATGATGATG 3720
OY 3721 ATCCATTCCTTGGAGACACCTTACTGTAATGATGATGATGATGATGATGATGATGATG 3780
| | | | |
DB 3721 ATCCATTCCTTGGAGACACCTTACTGTAATGATGATGATGATGATGATGATGATGATG 3780
OY 3781 GCTGGCTTCTGCTTCTGAGTTGACATTAATGATGATGATGATGATGATGATGATGATG 3840
| | | | |
DB 3781 GCTGGCTTCTGCTTCTGAGTTGACATTAATGATGATGATGATGATGATGATGATGATG 3840
OY 3841 TTTGTAATGAGCTTCCAGACTCTTGGCTTGGAGAGCGCTGTAGAGATCTTCAAGTCCA 3900
| | | | |
DB 3841 TTTGTAATGAGCTTCCAGACTCTTGGCTTGGAGAGCGCTGTAGAGATCTTCAAGTCCA 3900
OY 3901 TCATAGAAAAATGAAACACAGAGTGTCTGCTGATGATTTTGGGATACGCTCATCTT 3960
| | | | |
DB 3901 TCATAGAAAAATGAAACACAGAGTGTCTGCTGATGATTTTGGGATACGCTCATCTT 3960
OY 3961 TTAAGGATGCTTTCATCTAATTTGCGAGAGCTCAACAAAGATCAGCTCATAC 4020
| | | | |
DB 3961 TTAAGGATGCTTTCATCTAATTTGCGAGAGCTCAACAAAGATCAGCTCATAC 4020
OY 4021 TACATCAGCAAAATATATGCGCTTGTCTCTGACAAAGATATGTTTCTCTTGG 4080
| | | | |
DB 4021 TACATCAGCAAAATATATGCGCTTGTCTCTGACAAAGATATGTTTCTCTTGG 4080
OY 4081 AAACACCACTCATCTTGCATATAGCCGTGAAGATGATGATGATGATGATGATGATG 4140
| | | | |
DB 4081 AAACACCACTCATCTTGCATATAGCCGTGAAGATGATGATGATGATGATGATGATG 4140
OY 4141 TGTTCAAAAATTTGGAGAAAGTATTTAAATAAACCCTTAAATTTTATTCGACAAATAAA 4200
| | | | |
DB 4141 TGTTCAAAAATTTGGAGAAAGTATTTAAATAAACCCTTAAATTTTATTCGACAAATAAA 4200
```

Db 4141 TCTTACAAAATTGGACAAAGTATTTAATAAACTCTTAATTTTACTGACATMAAA 4200
QY 4201 ATTTTCTACAGATATTATTTAATGTTAACAGACAAATAATATGTCACGCACTTAAAAAAA 4260
Db 4201 ATCTTTCTACAGATATTATTTAATGTTAACAGACAAATAATATGTCACGCACTTAAAAAAA 4260
QY 4261 AAAAAAA 4268
Db 4261 AAAAAAA 4268

RESULT 2
AX34117 4268 bp DNA linear PAT 09-JAN-2002
LOCUS AX34117
DEFINITION Sequence 4626 from Patent WO0194629.
ACCESSION AX34117
VERSION AX34117.1 GI:18124836
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Plimates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Hortigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4626 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1..4268
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1199 a 964 c 1028 g 1077 t
ORIGIN
Query Match 100.0%; Score 4268; DB 6; Length 4268;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCAAGGACCACTTCTGCGTTTGAGATTGCTCCCAACACCCCGGCTGCTGCTTTC 60
Db 1 CCCAAGGACCACTTCTGCGTTTGAGATTGCTCCCAACACCCCGGCTGCTGCTTTC 60
QY 61 TCCATCCGACCCACCGGGGGGGGGGACACACAGTCGGGAGAGGGTTCCTTC 120
Db 61 TCCATCCGACCCACCGGGGGGGGGGACACACAGTCGGGAGAGGGTTCCTTC 120
QY 121 AAGTACGTGACGACGACGCGCTGCTGCTGAGCCCAACGCGAGCTGAAGCA 180
Db 121 AAGTACGTGACGACGACGCGCGGGGGGACACACAGTCGGGAGAGGGTTCCTTC 180
QY 181 TTGGCGCTAGTCATGCCCGTAGAGAAAGTGTGCAAGATGGATTAACTCCACATGAGA 240
Db 181 TTGGCGCTAGTCATGCCCGTAGAGAAAGTGTGCAAGATGGATTAACTCCACATGAGA 240
QY 241 TATGAAGAGAGACCGGGATTGTGATACCGTAAACATGTCAGCTGGGGCTTTATCTGCG 300
Db 241 TATGAAGAGAGACCGGGATTGTGATACCGTAAACATGTCAGCTGGGGCTTTATCTGCG 300
QY 301 CTGGTCTGCTGTCACCATGGCAACCTTGTCTCTGGCCCGGCTCTCTCAAGTTTATGTTAG 360
Db 301 CTGGTCTGCTGTCACCATGGCAACCTTGTCTCTGGCCCGGCTCTCTCAAGTTTATGTTAG 360
QY 361 GATACCATTTAGAGCCGGAAGAGCGCACCAACCAATATCTCTCAACCGAAGTG 420
Db 361 GATACCATTTAGAGCCGGAAGAGCGCACCAACCAATATCTCTCAACCGAAGTG 420
QY 421 TACGTCGCTGGCCAGGGAGATCGCTAGAGTGGCTCTCTGTTGAAGATGCCCGCTG 480
Db 421 TACGTCGCTGGCCAGGGAGATCGCTAGAGTGGCTCTCTGTTGAAGATGCCCGCTG 480
QY 481 ATCACTTGAGCTAAGGATGGGGTGCACTTGGGGCCCAACATAGACAGTCTTATTTGGG 540

Db 481 ATCACTTGAGCTAAGGATGGGGTGCACTTGGGGCCCAACATAGACAGTCTTATTTGGG 540
QY 541 GAGTACTTGCAGATATAAGGGCCACCGCTAGAGATCTCGGCTCTATGCTTACTGCC 600
Db 541 GAGTACTTGCAGATATAAGGGCCACCGCTAGAGATCTCGGCTCTATGCTTACTGCC 600
QY 601 AGTAGAGCTGTAGACAGTGAACCTTGGTACTTCAATGATGTAATGTACAGATGCCATGCA 660
Db 601 AGTAGAGCTGTAGACAGTGAACCTTGGTACTTCAATGATGTAATGTACAGATGCCATGCA 660
QY 661 TCCGAGATGATGAGATGACACCGATGGTGGGAAGATTTTGTCACTGAGACAGTAAAC 720
Db 661 TCCGAGATGATGAGATGACACCGATGGTGGGAAGATTTTGTCACTGAGACAGTAAAC 720
QY 721 AACCAAGAGACACCATTTACTGACACACACAGAAAGATGAAAGCGGCTCATGCTGTG 780
Db 721 AACCAAGAGACACCATTTACTGACACACAGAAAGATGAAAGCGGCTCATGCTGTG 780
QY 781 CCTGGCGCCCAACATGTCAGTTTGGCTGGCCAGCGGGGGGAACCAATGGCAACATG 840
Db 781 CCTGGCGCCCAACATGTCAGTTTGGCTGGCCAGCGGGGGGAACCAATGGCAACATG 840
QY 841 CGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGAGCATCGCATTTGAGGCTTACAAGSTA 900
Db 841 CGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGAGCATCGCATTTGAGGCTTACAAGSTA 900
QY 901 CGAAGACACACTGAGACCTCATTTATGCAAGTGTGTCTCCATCTGACAGAGGAATAT 960
Db 901 CGAAGACACACTGAGACCTCATTTATGCAAGTGTGTCTCCATCTGACAGAGGAATAT 960
QY 961 ACCTGTGTGTGAGAGATGAATACGGGTCCATCAATCAACATACACCTGATGTTGTG 1020
Db 961 ACCTGTGTGTGAGAGATGAATACGGGTCCATCAATCAACATACACCTGATGTTGTG 1020
QY 1021 GAGCGATCGCTTCACCGGCGCCATCTCCAAAGCCGAGCTCCGGAATGCTCCACAGTG 1080
Db 1021 GAGCGATCGCTTCACCGGCGCCATCTCCAAAGCCGAGCTCCGGAATGCTCCACAGTG 1080
QY 1081 GTTCGAGAGACGTACAGTTTGTCTGCAAGGTTTACAGTATGAGCCAGCCACATTCAG 1140
Db 1081 GTTCGAGAGACGTACAGTTTGTCTGCAAGGTTTACAGTATGAGCCAGCCACATTCAG 1140
QY 1141 TGGATCAAGACGTGGAAGAAAGACGACAGTAAATACGGGCGGAGGCTGCTACCTC 1200
Db 1141 TGGATCAAGACGTGGAAGAAAGACGACAGTAAATACGGGCGGAGGCTGCTACCTC 1200
QY 1201 AAGGTTCTCAAGCGCGCGGTGTTAACACACGAGACAAAGAGATGAGTCTCTATATT 1260
Db 1201 AAGGTTCTCAAGCGCGCGGTGTTAACACACGAGACAAAGAGATGAGTCTCTATATT 1260
QY 1261 GGGAAATGAACCTTTGAGGAGCGCTGGGAAATATACGTGCTGGCGGTAAATCTATTGGG 1320
Db 1261 GGGAAATGAACCTTTGAGGAGCGCTGGGAAATATACGTGCTGGCGGTAAATCTATTGGG 1320
QY 1321 ATATCTTTCACTCTCATAGTTTGACAGTTTGTGCAAGCGCTGGAAGAGAAAGAGATT 1380
Db 1321 ATATCTTTCACTCTCATAGTTTGACAGTTTGTGCAAGCGCTGGAAGAGAAAGAGATT 1380
QY 1381 ACAGCTTCCCAAGATACCTGAGAGATAGCCATTTACTGCTAAGGGTCTTCTAATCGGC 1440
Db 1381 ACAGCTTCCCAAGATACCTGAGAGATAGCCATTTACTGCTAAGGGTCTTCTAATCGGC 1440
QY 1441 TGTATGGTGTAAACAGTCACTGTGGCCGAATGAAGAACACGACAAAGAGCAGACTTC 1500
Db 1441 TGTATGGTGTAAACAGTCACTGTGGCCGAATGAAGAACACGACAAAGAGCAGACTTC 1500
QY 1501 AGCAGCCAGCGGCTGTGCAACAGTGAACCAAGTATCCCTCGGGAGACAGGTAAAC 1560
Db 1501 AGCAGCCAGCGGCTGTGCAACAGTGAACCAAGTATCCCTCGGGAGACAGGTAAAC 1560
QY 1561 GTTTGGCTGAGTTCACGCTCTCATGAACTCCAAACCCCGGTGGGAGATTAACACA 1620

Db 1561 GTTTCGGCTGAGTCCAGTCTCCATGCACTCCACACCCCGTGGTAGAGATAACACA 1620
OY 1621 CGCCTCTCTTCACGCGAGACACCCCATGCTGGCAGGGGTCTCCGAGTATGAATTCGA 1680
Db 1621 CGCCTCTCTTCACGCGAGACACCCCATGCTGGCAGGGGTCTCCGAGTATGAATTCGA 1680
OY 1681 GAGACCCCAAAATGGGAGTTTCCAAAGATTAAGTGAACACTGGGCAAGCCCTGGAGAA 1740
Db 1681 GAGACCCCAAAATGGGAGTTTCCAAAGATTAAGTGAACACTGGGCAAGCCCTGGAGAA 1740
OY 1741 GGTTCCTTTGGGCAAGTGTGTCATGGCGAAGCACTGGGAAATTTGCAAAAGACACCCCAAG 1800
Db 1741 GGTTCCTTTGGGCAAGTGTGTCATGGCGAAGCACTGGGAAATTTGCAAAAGACACCCCAAG 1800
OY 1801 GAGCGGTCACCGTGGCCGCTGAAGATTTGAAAGATGATGCACAGAGAAACCTTTCT 1860
Db 1801 GAGCGGTCACCGTGGCCGCTGAAGATTTGAAAGATGATGCACAGAGAAACCTTTCT 1860
OY 1861 GATCTGGTTCAGAGATGAGATGAATGAATGATTTGGAAACACAGAAATATCATTAAT 1920
Db 1861 GATCTGGTTCAGAGATGAGATGAATGAATGATTTGGAAACACAGAAATATCATTAAT 1920
OY 1921 CTTCCTGGACCTGTCACACAGAGATGGGCTCTCTATGTCATAGTTGATGGCTCTAAA 1980
Db 1921 CTTCCTGGACCTGTCACACAGAGATGGGCTCTCTATGTCATAGTTGATGGCTCTAAA 1980
OY 1981 GGCACCTCCGAGAAATCCTCCGAGCCGAGGACCCCGGAGTGAATCTCTATGAC 2040
Db 1981 GGCACCTCCGAGAAATCCTCCGAGCCGAGGACCCCGGAGTGAATCTCTATGAC 2040
OY 2041 ATTACCGTCTCTGAGGAGAGATGACCTTCAAGACCTTGGTGTGTCACACCTTACAG 2100
Db 2041 ATTACCGTCTCTGAGGAGAGATGACCTTCAAGACCTTGGTGTGTCACACCTTACAG 2100
OY 2101 CTGGCCAGAGGATGAGATGCTTGGCTCCCAAAATGATTCATGAGATTTAGAGGCC 2160
Db 2101 CTGGCCAGAGGATGAGATGCTTGGCTCCCAAAATGATTCATGAGATTTAGAGGCC 2160
OY 2161 AGAAATGTTTGGTAAACAGAAACAAATGTGATGAAAAATAGCAGACTTGGACCTGCAG 2220
Db 2161 AGAAATGTTTGGTAAACAGAAACAAATGTGATGAAAAATAGCAGACTTGGACCTGCAG 2220
OY 2221 GATATCAACATATAGACTATTACAAAAGACCAATGGGGGCTTCCAGTCAAGTGG 2280
Db 2221 GATATCAACATATAGACTATTACAAAAGACCAATGGGGGCTTCCAGTCAAGTGG 2280
OY 2281 ATGGCTCCAGAAACCCCTGTTTGTATAGATATACATCATCAGATGATGCTGGCTTTC 2340
Db 2281 ATGGCTCCAGAAACCCCTGTTTGTATAGATATACATCATCAGATGATGCTGGCTTTC 2340
OY 2341 GGGGTGTTAATGGGAGATCTTCACTTTAGGGGCTCCGCCATCCAGAGGATTCGGTG 2400
Db 2341 GGGGTGTTAATGGGAGATCTTCACTTTAGGGGCTCCGCCATCCAGAGGATTCGGTG 2400
OY 2401 GAGGAACCTTTTAACTGTGTAAGGAAGACAGAAATGATTAAGCAGACCAACTGCACC 2460
Db 2401 GAGGAACCTTTTAACTGTGTAAGGAAGACAGAAATGATTAAGCAGACCAACTGCACC 2460
OY 2461 AAGCAACTATACATGATGATGAGGACCTGTGGCATGACAGTGCCCTCCAGAGACCAAG 2520
Db 2461 AAGCAACTATACATGATGATGAGGACCTGTGGCATGACAGTGCCCTCCAGAGACCAAG 2520
OY 2521 TTCAACGACTGGTAGAAGACTTGGATGCAATTTCTACCTCTACAAACCAATAGAGAAATG 2580
Db 2521 TTCAACGACTGGTAGAAGACTTGGATGCAATTTCTACCTCTACAAACCAATAGAGAAATG 2580
OY 2581 TTGGAGCTCAGCCAACTCTCGAAGAGATTCACCTAGTTACCTCGACAGAAAGTTT 2640
Db 2581 TTGGAGCTCAGCCAACTCTCGAAGAGATTCACCTAGTTACCTCGACAGAAAGTTT 2640
OY 2641 TCTTCTTCAAGGAGATGATTTCTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2700
Db 2641 TCTTCTTCAAGGAGATGATTTCTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2700

OY 2701 CTTAGATTCACACATTAACGGCAGTGTAAAAACATGAATGACTGTGCTGCTGCC 2760
Db 2701 CTTAGATTCACACATTAACGGCAGTGTAAAAACATGAATGACTGTGCTGCTGCC 2760
OY 2761 CAACAGAGACGACCTGGGAACCTAGCTACACTGAGAGGAGACCATGCTGCCAGAGC 2820
Db 2761 CAACAGAGACGACCTGGGAACCTAGCTACACTGAGAGGAGACCATGCTGCCAGAGC 2820
OY 2821 TTGTGCTCCACTTGTATATATGATCAGAGAGTAAATATTTGGAAAAATGATACGA 2880
Db 2821 TTGTGCTCCACTTGTATATATGATCAGAGAGTAAATATTTGGAAAAATGATACGA 2880
OY 2881 TATGTGAAAGATTTATACGTGAAACCTTGAATCTTCCCGAGAGAGAAAGTGT 2940
Db 2881 TATGTGAAAGATTTATACGTGAAACCTTGAATCTTCCCGAGAGAGAAAGTGT 2940
OY 2941 TCTGAGCAGTGCAGCTGCCCAAGCCACATGTAACCCCTCTCACCTGGCGGCTTCTG 3000
Db 2941 TCTGAGCAGTGCAGCTGCCCAAGCCACATGTAACCCCTCTCACCTGGCGGCTTCTG 3000
OY 3001 GCTGTGACCACTAGACCTCAAGGTGACGTGCGTCTGCTCTCTTGAATTTTGA 3060
Db 3001 GCTGTGACCACTAGACCTCAAGGTGACGTGCGTCTGCTCTCTTGAATTTTGA 3060
OY 3061 TAAATGAGAGATTTATGTCAGCAGACACATTAACAGAGCAAAATGACATATAGTGC 3120
Db 3061 TAAATGAGAGATTTATGTCAGCAGACACATTAACAGAGCAAAATGACATATAGTGC 3120
OY 3121 TGGATGATGAAATATATTCAAATATGATATATATATATATATATATATATATAT 3180
Db 3121 TGGATGATGAAATATATTCAAATATGATATATATATATATATATATATATATATAT 3180
OY 3181 TATTTTGTATGATTTAAATGATGATGCCAATGACCTAGAAAAATGCTCTCTT 3240
Db 3181 TATTTTGTATGATTTAAATGATGATGCCAATGACCTAGAAAAATGCTCTCTT 3240
OY 3241 TTTTAACTATTTCTTAAATGCTGTCTTACATATATTTCTTAAATTTTACAGAGCA 3300
Db 3241 TTTTAACTATTTCTTAAATGCTGTCTTACATATATTTCTTAAATTTTACAGAGCA 3300
OY 3301 GAGGTGAAAAAATACTTGTCTTCAAGGAAAAATGATTAACGTTATATTAAT 3360
Db 3301 GAGGTGAAAAAATACTTGTCTTCAAGGAAAAATGATTAACGTTATATTAAT 3360
OY 3361 TGGTAAATATCAAAACATTAATCATTTATAGTTTTTTTGTAAATTAAGTGCAATTTCT 3420
Db 3361 TGGTAAATATCAAAACATTAATCATTTATAGTTTTTTTGTAAATTAAGTGCAATTTCT 3420
OY 3421 ATGCAGGACGACAGCAGACTAGTTAATCTATTTGCTGGACTTAATGATCAGATCC 3480
Db 3421 ATGCAGGACGACAGCAGACTAGTTAATCTATTTGCTGGACTTAATGATCAGATCC 3480
OY 3481 TTTGAAAAAGAAATATTTCAATATATGACTAATTTGGGAAAAATGAAGTTTGTAT 3540
Db 3481 TTTGAAAAAGAAATATTTCAATATATGACTAATTTGGGAAAAATGAAGTTTGTAT 3540
OY 3541 TTGTGTTTAAATGCTGTGTCAGAGATTTCTTAGACCTCTTAAAGCCCATATTTAA 3600
Db 3541 TTGTGTTTAAATGCTGTGTCAGAGATTTCTTAGACCTCTTAAAGCCCATATTTAA 3600
OY 3601 AAGAACTATTCATAGGAAGTGTTCATTTTGGTGCACACCCCTGTATTAACGCAAG 3660
Db 3601 AAGAACTATTCATAGGAAGTGTTCATTTTGGTGCACACCCCTGTATTAACGCAAG 3660
OY 3661 CAAGCTCTAAGCTGCACTTCCCAAGATTAATGATACAGCTGCTTTAAAGATGCTTA 3720
Db 3661 CAAGCTCTAAGCTGCACTTCCCAAGATTAATGATACAGCTGCTTTAAAGATGCTTA 3720
OY 3721 ATCCATTCCTTGAGAGACACTTATGTTGAATGATACAGAAATGCTGCTCTGCA 3780
Db 3721 ATCCATTCCTTGAGAGACACTTATGTTGAATGATACAGAAATGCTGCTCTGCA 3780

1
QY 1201 AAGTTCCTCAAGGCCCGCGTGTTAACACGACGACAAAGATTAAGCTTCCTATATT 1260
DB 1201 AAGTTCCTCAAGGCCCGCGTGTTAACACGACGACAAAGATTAAGCTTCCTATATT 1260
QY 1261 CGGAATGTAACCTTTTGAAGACGCTGGGGAATATAGCTGGCGGTAACTTATTTGG 1320
DB 1261 CGGAATGTAACCTTTTGAAGACGCTGGGGAATATAGCTGGCGGTAACTTATTTGG 1320
QY 1321 ATATCTTTTACTCTGCATGTTGACAGTTCTGCCAGCGCTGGAAAGAGAAAGAGATT 1380
DB 1321 ATATCTTTTACTCTGCATGTTGACAGTTCTGCCAGCGCTGGAAAGAGAAAGAGATT 1380
QY 1381 AAGGCTTCCCGAGTACTGAGGAGATAGCCATTACTGCATAGGGTCTTTTAATGCC 1440
DB 1381 AAGGCTTCCCGAGTACTGAGGAGATAGCCATTACTGCATAGGGTCTTTTAATGCC 1440
QY 1441 TGTATGCTGTAACAGTACTCTGTCGGAATGAAGAACAGACGAAGAAGCCAGACTTC 1500
DB 1441 TGTATGCTGTAACAGTACTCTGTCGGAATGAAGAACAGACGAAGAAGCCAGACTTC 1500
QY 1501 AGCAGCCAGCCGGCTGTGCACAAAGCTGACCAACGTAATCCCTCGGAGACAGGTACA 1560
DB 1501 AGCAGCCAGCCGGCTGTGCACAAAGCTGACCAACGTAATCCCTCGGAGACAGGTACA 1560
QY 1561 GTTTGGGCTGAGTCCAGCTCCATGACCTCCACACACCCCGCTGGTGAAGATTAACACA 1620
DB 1561 GTTTGGGCTGAGTCCAGCTCCATGACCTCCACACACCCCGCTGGTGAAGATTAACACA 1620
QY 1621 CGCCTCTCTTCAACGAGCAGACACCCCATGCTGGCAGGGGTCTCGAGATGTAACCTCA 1680
DB 1621 CGCCTCTCTTCAACGAGCAGACACCCCATGCTGGCAGGGGTCTCGAGATGTAACCTCA 1680
QY 1681 GAGGAGCCAAATTTGGAGCTTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
DB 1681 GAGGAGCCAAATTTGGAGCTTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
QY 1741 GGTTCCTTTGGGCAAGTGTGTCATGGGGAAGCAGTGGGAATTGACAAACAGAACCCCAAG 1800
DB 1741 GGTTCCTTTGGGCAAGTGTGTCATGGGGAAGCAGTGGGAATTGACAAACAGAACCCCAAG 1800
QY 1801 GAGGCGGTACCCGTGGCCCTGGAAGATGTTGAAAGATGATGTCACAGAGAAAGACCTTCT 1860
DB 1801 GAGGCGGTACCCGTGGCCCTGGAAGATGTTGAAAGATGATGTCACAGAGAAAGACCTTCT 1860
QY 1861 GATCTGGTGTGAGATGAGATGATGAAGATGATTGGAAACACAGAAATTCATTAAT 1920
DB 1861 GATCTGGTGTGAGATGAGATGATGAAGATGATTGGAAACACAGAAATTCATTAAT 1920
QY 1921 CTTCTTGGAGCCTGACACAGAGATGGGCTCTCTATGTCATGTTGAGATGCCCTTAA 1980
DB 1921 CTTCTTGGAGCCTGACACAGAGATGGGCTCTCTATGTCATGTTGAGATGCCCTTAA 1980
QY 1981 GCGAACCCTCCGGAATTAACCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCTATGAC 2040
DB 1981 GCGAACCCTCCGGAATTAACCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCTATGAC 2040
QY 2041 ATTTAACCGTGTCTGAGAGAGATGAACCTTCAAGGACTTGGTGTGATGCACTTACACAG 2100
DB 2041 ATTTAACCGTGTCTGAGAGAGATGAACCTTCAAGGACTTGGTGTGATGCACTTACACAG 2100
QY 2101 CTGGCCAGAGGAGTACTTGGCTTCCCAAAATGATTAATGATGAGATTACAGAG 2160
DB 2101 CTGGCCAGAGGAGTACTTGGCTTCCCAAAATGATTAATGATGAGATTACAGAG 2160
QY 2161 AGAAATGTTTTGTGTAACGAAACAAATGTGATGAATATGACAGCTTTGGACTGCCAGA 2220
DB 2161 AGAAATGTTTTGTGTAACGAAACAAATGTGATGAATATGACAGCTTTGGACTGCCAGA 2220
QY 2221 GATATCAACATATATGACTATTATACAAAAGACCAACATGGCGGCTTCCAGTCAAGTGG 2280
DB 2221 GATATCAACATATATGACTATTATACAAAAGACCAACATGGCGGCTTCCAGTCAAGTGG 2280
QY 2281 ATGGCTCAGAAAGCCCTGTTTGTATAGATATACACTCATAGAGTGTCTGCTTTC 2340

DB 2281 ATGGCTCAGAAAGCCCTGTTGATAGATATACACTCATCAGAGTATGTGTCCTTC 2340
QY 2341 GGGGTATATATGTTGGAGATCTTCACTTTAAGGGGCTGCCCTACCCAGGATTCGGTG 2400
DB 2341 GGGGTATATATGTTGGAGATCTTCACTTTAAGGGGCTGCCCTACCCAGGATTCGGTG 2400
QY 2401 GAGGAACCTTTTAAGTGTCTGAAAGGAAGACAGAAATGATTAAGCCAACTGCCAAC 2460
DB 2401 GAGGAACCTTTTAAGTGTCTGAAAGGAAGACAGAAATGATTAAGCCAACTGCCAAC 2460
QY 2461 AAGGAACCTGATGATGATGAGGAGCTGTGGCATGACAGTCCCTCCAGAGACCAAG 2520
DB 2461 AAGGAACCTGATGATGATGAGGAGCTGTGGCATGACAGTCCCTCCAGAGACCAAG 2520
QY 2521 TTCAAGCACTTGGTGAACACTTGGATGCAATTTCTCACTCTACAAACATAGAGAAATC 2580
DB 2521 TTCAAGCACTTGGTGAACACTTGGATGCAATTTCTCACTCTACAAACATAGAGAAATC 2580
QY 2581 TTGAGACTGAGCCAACTCTCGAACAGTATTCAGTATACCTGACGACCAAGAGTTCT 2640
DB 2581 TTGAGACTGAGCCAACTCTCGAACAGTATTCAGTATACCTGACGACCAAGAGTTCT 2640
QY 2641 TGTCTTTCAGAGATGATTTCTGTTTTCTCGAGACCCCATGCTTACGAACCATGCTT 2700
DB 2641 TGTCTTTCAGAGATGATTTCTGTTTTCTCGAGACCCCATGCTTACGAACCATGCTT 2700
QY 2701 GCTCAGTATCCACATTAACGGGAGTGTAAACATGATATAGTCTGTGCTGCTCC 2760
DB 2701 GCTCAGTATCCACATTAACGGGAGTGTAAACATGATATAGTCTGTGCTGCTCC 2760
QY 2761 CAAAGAGCAGCAGTGGGAACCTAGCTAGCTAGCAGAGGAGACATGCTCCCAAGC 2820
DB 2761 CAAAGAGCAGCAGTGGGAACCTAGCTAGCTAGCAGAGGAGACATGCTCCCAAGC 2820
QY 2821 TTGCTGTCTCCACTTGTATATATGATCAGAGAGTAAATTAATGAAAGTAAATCACA 2880
DB 2821 TTGCTGTCTCCACTTGTATATATGATCAGAGAGTAAATTAATGAAAGTAAATCACA 2880
QY 2881 TATGTGTAAGATTAATACAGTTGAAACCTGTATCTTCCCGAGAGAGAAAGGTT 2940
DB 2881 TATGTGTAAGATTAATACAGTTGAAACCTGTATCTTCCCGAGAGAGAAAGGTT 2940
QY 2941 TCTGAGCAGTGGACTGCCACAAAGCCACCATGTAACCCCTGACCTGCCGTCTTG 3000
DB 2941 TCTGAGCAGTGGACTGCCACAAAGCCACCATGTAACCCCTGACCTGCCGTCTTG 3000
QY 3001 GCTGTGAGCAGTACGACTCAAGGTGAGCTGCTGCTTCCCTGTTAAATTTGTA 3060
DB 3001 GCTGTGAGCAGTACGACTCAAGGTGAGCTGCTGCTTCCCTGTTAAATTTGTA 3060
QY 3061 TAAATGAGAGATTAATATGTCAGCACACACTTACAGACACAAATGAGTATATGAGTGC 3120
DB 3061 TAAATGAGAGATTAATATGTCAGCACACACTTACAGACACAAATGAGTATATGAGTGC 3120
QY 3121 TGGATGTATGTAATATATTCAAATATATATATATATATATATATATATATATATATAT 3180
DB 3121 TGGATGTATGTAATATATTCAAATATATATATATATATATATATATATATATATATAT 3180
QY 3181 TATTTTGTATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
DB 3181 TATTTTGTATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
QY 3241 TTTTAAATGATTTTGTAAATGCTGCTTATACATATATTTCTTAAATTTTACCGAGACA 3300
DB 3241 TTTTAAATGATTTTGTAAATGCTGCTTATACATATATTTCTTAAATTTTACCGAGACA 3300
QY 3301 GAGGTGGAAGAAATACCTTTGCTTCAGGAAATGATATTAACGTTAATTAATTAAT 3360
DB 3301 GAGGTGGAAGAAATACCTTTGCTTCAGGAAATGATATTAACGTTAATTAATTAAT 3360
QY 3361 TGTATATATACAAACATTAATCATTTATAGTTTTTTTCTAATTTAAGTGCATTTCT 3420
DB 3361 TGTATATATACAAACATTAATCATTTATAGTTTTTTTCTAATTTAAGTGCATTTCT 3420

QY	421	TACGTGGCTGCCCAAGGGAGCTGCTAGAGTGGCTGCTGCTGTTGAAAGATGCCGCGTG	480
Db	421	TACGTGGCTGCCCAAGGGAGAGTGGCTAGAGTGGCTGCTGCTGTTGAAAGATGCCGCGTG	480
QY	481	ATCAGTGGACATAAGATAGTGGGTGACTTTGGGGGCCCAACAAATAGACAGTCTTATTTGGG	540
Db	481	ATCAGTGGACATAGAGATGGGTGACTTTGGGGGCCCAACAAATAGAGTGGCTTATTTGGG	540
QY	541	GAGTACTTGCAGATAAAGGGCGCCACGGCTTAGAGACTGCCGCTCTATCTGTTTACTTGGC	600
Db	541	GAGTACTTGCAGATAAAGGGCGCCACGGCTTAGAGACTTGCGGCTCTATGTTTACTGGC	600
QY	601	AGTAGACTCTAGACAGTGAATCTTGACTTCAATGGTGAATGTCAACAGATGCAATCTCA	660
Db	601	AGTAGACTCTAGACAGTGAATCTTGACTTCAATGGTGAATGTCAACAGATGCAATCTCA	660
QY	661	TCCGGAGATGATAGAGATGACACCGATGTTGCGGAAGATTTTGTCAGTGAAGCACTAAC	720
Db	661	TCCGGAGATGATAGAGATGACACCGATGTTGCGGAAGATTTTGTCAGTGAAGCACTAAC	720
QY	721	AACCAAGAGACCACTACTGAGCCACACAGAAAAGATGCAAAAAGCGGCTCCATGCTGTG	780
Db	721	AACCAAGAGACCACTACTGAGCCACACAGAAAAGATGCAAAAAGCGGCTCCATGCTGTG	780
QY	781	CCTGGCGCCCAACACTGTCAAATTTTCGTGCCACGCGGGGGGAAACCAATGCCAACATG	840
Db	781	CCTGGCGCCCAACACTGTCMAATTTTCGTGCCACGCGGGGGGAAACCAATGCCAACATG	840
QY	841	CGGTGGCTGAAAAAGCGAAGAGATTTAAGCAGAGAGCATGCATTGAGGCTTACAAGATA	900
Db	841	CGGTGGCTGAAAAAGCGGAGAGAGATTTAAGCAGAGAGCATGCATTGAGGCTTACAAGATA	900
QY	901	CGAAACCCAGCACTGAGGAGCTCATTTATGGAAGTGTGTCCATCTGACAAAGGAATTTAT	960
Db	901	CGAAACCCAGCACTGAGAGCTCATTTATGGAAGTGTGTCCATCTGACAAAGGAATTTAT	960
QY	961	ACCTTGTGTGGAGATGAATACGGGTCCATCAATCACACGTAACCACTGGATGTTGTG	1020
Db	961	ACCTTGTGTGGAGATGAATACGGGTCCATCAATCACACGTAACCACTGGATGTTGTG	1020
QY	1021	GAGCATAGCTGCACCGGGCCATCTTCCAAAGCCGGAGCTGCCGGCAATGCTCTCACAGTG	1080
Db	1021	GAGCATAGCTGCACCGGGCCATCTTCCAAAGCCGGAGCTGCCGGCAATGCTCTCACAGTG	1080
QY	1081	GTCGGAGAGACGTAGAGTGTGTCGAAGGTTTACAGTGAATGCCAGCCCACTCCAG	1140
Db	1081	GTCGGAGAGACGTAGAGTGTGTCGAAGGTTTACAGTGAATGCCAGCCCACTCCAG	1140
QY	1141	TGGAACAAGACGTCGTGAAAAAGACGGCAGTAAATACGGGCCGAGCGCTGCCCTACCTC	1200
Db	1141	TGGAACAAGACGTCGTGAAAAAGACGGCAGTAAATACGGGCCGAGCGCTGCCCTACCTC	1200
QY	1201	AAGGTTTCAAGGGCGCGGCTGTTTAAACACCAAGCAAGAGAGTTGAGGTTGTCATATTT	1260
Db	1201	AAGGTTTCAAGGGCGCGGCTGTTTAAACACCAAGCAAGAGAGTTGAGGTTGTCATATTT	1260
QY	1261	CGGAATGTAACCTTTTGAGACGCTGGGGAATATACGTGCTTGAGCGGTAAATCTTATTTGGG	1320
Db	1261	CGGAATGTAACCTTTTGAGACGCTGGGGAATATATACGTGCTTGAGCGGTAAATCTTATTTGGG	1320
QY	1321	ATATCCTTTTACTCTGATGTTGACAGTTCCTGCCAGCGCTCGGAAGAAAGAAAGAGATT	1380
Db	1321	ATATCCTTTTACTCTGATGTTGACAGTTCCTGCCAGCGCTCGGAAGAAAGAAAGAGATT	1380
QY	1381	ACAGCTTCCCAAGACTACCTGGAAGATAGCCATTTACTGCATAGGGGTCTTCTTAATGCC	1440
Db	1381	ACAGCTTCCCAAGACTACCTGGAAGATAGCCATTTACTGCATAGGGGTCTTCTTAATGCC	1440
QY	1441	TGTATGTTGTAACAGTCACTCGTGGTGGCAATGAAGAACACAGACCAAGAGCCAGACTTC	1500
Db	1441	TGTATGTTGTAACAGTCACTCGTGGTGGCAATGAAGAACACAGACCAAGAGCCAGACTTC	1500

Qy	1501	AGAGCGACACCGGCGTGTGCACAACTGCACAAACGATATCCCGCTGGGAGACAGGTAA	1560
Db	1501	AGCAAGCGACCGGGCTGTGCACAACTGCACAAACGATATCCCGCTGGGAGACAGGTAA	1560
Qy	1561	GTTCGGCGTGAATCCAGCTCCTCCATGAACCTCCAAACCGCCGGTGGTGAGATPACACA	1620
Db	1561	GTTCGGCGTGAATCCAGCTCCTCCATGAACCTCCAAACCGCCGGTGGTGAGATPACACA	1620
Qy	1621	CGCTCTCTTCAAGGGCACAGACACCCCATGCTGGCAGGGGTCTCCGATGATCACTTCCA	1680
Db	1621	CGCTCTCTTCAAGGGCACAGACACCCCATGCTGGCAGGGGTCTCCGATGATCACTTCCA	1680
Qy	1681	GAGGACCCCAAAATGGGAATTTCCAAAGATATAGCTGACACTGGGCAAGCCCTGGGAA	1740
Db	1681	GAGGACCCCAAAATGGGAATTTCCAAAGATATAGCTGACACTGGGCAAGCCCTGGGAA	1740
Qy	1741	GCTTCGTTGGGCAAGTGTGTCATGGCGGAAGCAGTGGGAATTTGACAAAGACAAAGCC	1800
Db	1741	GCTTCGTTGGGCAAGTGTGTCATGGCGGAAGCAGTGGGAATTTGACAAAGACAAAGCC	1800
Qy	1801	GAGGGGGTCCACCGTGGCCGTGAATGTTTAAAGATGATGCCACAGAGAAAGACCTTTCT	1860
Db	1801	GAGGGGGTCCACCGTGGCCGTGAATGTTTAAAGATGATGCCACAGAGAAAGACCTTTCT	1860
Qy	1861	GATCTGATGTACAGAGATGAGAGATGATGAATGATTTGGGAAACACAGAAATATCTAAAT	1920
Db	1861	GATCTGATGTACAGAGATGAGAGATGATGAATGATTTGGGAAACACAGAAATATCTAAAT	1920
Qy	1921	CTTCTTGGAGCGCTGCACACAGAGATGGCGCTCTGTATGTATGATTTGAGTATGCCCTAA	1980
Db	1921	CTTCTTGGAGCGCTGCACACAGAGATGGCGCTCTGTATGTATGATTTGAGTATGCCCTAA	1980
Qy	1981	GGCAACCTCCGAGAAATACCTCCGAGCCCGGAGGCGCACCCGGATGAGATCCTATGAC	2040
Db	1981	GGCAACCTCCGAGAAATACCTCCGAGCCCGGAGGCGCACCCGGATGAGATCCTATGAC	2040
Qy	2041	ATTAAACCGTGTCTGTGAGAGACAGATGACCTTCAAGAGCTTGGTGTACACCTACAG	2100
Db	2041	ATTAAACCGTGTCTGTGAGAGACAGATGACCTTCAAGAGCTTGGTGTACACCTACAG	2100
Qy	2101	CTGGCCAGAGCGATGAGATGCTGGGCTGCCAAAAATGATTCATGCGAGATTTAGCAGCC	2160
Db	2101	CTGGCCAGAGCGATGAGATGCTGGGCTGCCAAAAATGATTCATGCGAGATTTAGCAGCC	2160
Qy	2161	AGAAATGTTTTGGTACAGAAAAACAATGTGATGAAATAGCAAGCTTTGACCTGCCAGA	2220
Db	2161	AGAAATGTTTTGGTACAGAAAAACAATGTGATGAAATAGCAAGCTTTGACCTGCCAGA	2220
Qy	2221	GATATCAACATATAGACTTTTACAAAAAGACCAACATGGGCGGCTTCCAGTCAAGTGG	2280
Db	2221	GATATCAACATATAGACTTTTACAAAAAGACCAACATGGGCGGCTTCCAGTCAAGTGG	2280
Qy	2281	ATGGCTCCAGAGCCCGTTTGATAGATATACCTTCATCAGAGATGTGTGCTCTTC	2340
Db	2281	ATGGCTCCAGAGCCCGTTTGATAGATATACCTTCATCAGAGATGTGTGCTCTTC	2340
Qy	2341	GGGGGTAAATGTGGGAGATCTTCACTTTAAGGGGCTGGCCCTACCCAGGATTTCCCGTG	2400
Db	2341	GGGGGTAAATGTGGGAGATCTTCACTTTAAGGGGCTGGCCCTACCCAGGATTTCCCGTG	2400
Qy	2401	GAGGAACTTTTAAAGCGCTGGAAGAAAGACACATGAGTAAGCCAGCCCACTGCACG	2460
Db	2401	GAGGAACTTTTAAAGCGCTGGAAGAAAGACACATGAGTAAGCCAGCCCACTGCACG	2460
Qy	2461	AAGCAACTGTATCATGATGATGAGGAGCTTGTGGCATGCAATGCTCCCAAGACCAAGC	2520
Db	2461	AAGCAACTGTATCATGATGATGAGGAGCTTGTGGCATGCAATGCTCCCAAGACCAAGC	2520
Qy	2521	TTTCAAGCAGTTGGTAAAGACTGGTATGCAATTCATCTCACAACCAATGAGGAATAC	2580
Db	2521	TTTCAAGCAGTTGGTAAAGACTGGTATGCAATTCATCTCACAACCAATGAGGAATAC	2580
Qy	2581	TTTGACCTCAAGCAACCTCTCGAACAGTATTCACCTAGTTACCTGTGACACAAAGTTAT	2640

```

Db 2581 TTGGACCTAGCCAACTCTGACACGATTAATCACTAGTACCCTGACCAAGAACTCT 2640
Oy 2641 TCTTCTTCAGAGATGATCTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTT 2700
Db 2641 TCTTCTTCAGAGATGATCTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTT 2700
Oy 2701 CCTCACTATCCACATTAAGCGCAGTGTAAACATGATACGTGTCTGCTGTCC 2760
Db 2701 CCTCACTATCCACATTAAGCGCAGTGTAAACATGATACGTGTCTGCTGTCC 2760
Oy 2761 CAAAGGAGACAGACACTGGGACCTTACCTACAGAGAGAGACCATCTCCAGAC 2820
Db 2761 CAAAGGAGACAGACACTGGGACCTTACCTACAGAGAGAGACCATCTCCAGAC 2820
Oy 2821 TTTCTCTCTCAGCTTATATATGATCAGAGAGATAAATTTGAAAAAGTAATCAGCA 2880
Db 2821 TTTCTCTCTCAGCTTATATATGATCAGAGAGATAAATTTGAAAAAGTAATCAGCA 2880
Oy 2881 TATGTGTAAGATTTTATACAGTTGAAACCTGTGATCTTCCAGAGAGAGAAAGTT 2940
Db 2881 TATGTGTAAGATTTTATACAGTTGAAACCTGTGATCTTCCAGAGAGAGAAAGTT 2940
Oy 2941 TCTGGAGAGAGTGGAGTGGCCAGACCATGTAACCCCTCAGCTGCGCTGCTTG 3000
Db 2941 TCTGGAGAGAGTGGAGTGGCCAGACCATGTAACCCCTCAGCTGCGCTGCTTG 3000
Oy 3001 GCTGTGAGCAGTAGAGACTGCAAGGTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Db 3001 GCTGTGAGCAGTAGAGACTGCAAGGTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Oy 3061 TAATTTGAGAGATTTATGTCAGCAGACACTTACAGAGCAAAATGACATATAGTGC 3120
Db 3061 TAATTTGAGAGATTTATGTCAGCAGACACTTACAGAGCAAAATGACATATAGTGC 3120
Oy 3121 TGGATGATGTAATATATCAATTAATGATATATATATATATATATATATATATAT 3180
Db 3121 TGGATGATGTAATATATCAATTAATGATATATATATATATATATATATATATAT 3180
Oy 3181 TATTTTGTATGATTTTAAATGATGTCCTCAATGACCTACAAAATGCTCTCTT 3240
Db 3181 TATTTTGTATGATTTTAAATGATGTCCTCAATGACCTACAAAATGCTCTCTT 3240
Oy 3241 TTTTAAATAGTATTTGCTAAATGCTGTTTACACATATTTCTTAAATTTTACCCGCA 3300
Db 3241 TTTTAAATAGTATTTGCTAAATGCTGTTTACACATATTTCTTAAATTTTACCCGCA 3300
Oy 3301 GAGGTGAAAAATACCTTTGCTTACAGGAAAAATGATTAACGTTAATTAATTAAT 3360
Db 3301 GAGGTGAAAAATACCTTTGCTTACAGGAAAAATGATTAACGTTAATTAATTAAT 3360
Oy 3361 TGGTAATATACAAAACAATTAATCAATTAATTTTGTGTAATTAATTAATTAATTA 3420
Db 3361 TGGTAATATACAAAACAATTAATCAATTAATTTTGTGTAATTAATTAATTAATTA 3420
Oy 3421 ATGAGGACAGCAGACAGACTAGTAACTATGCTGAGCTTAACAGTATACAGATCC 3480
Db 3421 ATGAGGACAGCAGCAGACAGACTAGTAACTATGCTGAGCTTAACAGTATACAGATCC 3480
Oy 3481 TTTGAAAAAGAAATATTTACAAATATAGCTAATTTGGGAAAAATGAAGTTTGAATTA 3540
Db 3481 TTTGAAAAAGAAATATTTACAAATATAGCTAATTTGGGAAAAATGAAGTTTGAATTA 3540
Oy 3541 TTTGCTTTAAATGCTGCTGTCACAGCATGTTCTTACAGCTCCAAATGGCCCATTTAA 3600
Db 3541 TTTGCTTTAAATGCTGCTGTCACAGCATGTTCTTACAGCTCCAAATGGCCCATTTAA 3600
Oy 3601 AAGAACTCATTCATAGGAAGGTGTTTATTTGCTGCAACCTGTCAATTAAGTCAAG 3660
Db 3601 AAGAACTCATTCATAGGAAGGTGTTTATTTGCTGCAACCTGTCAATTAAGTCAAG 3660
Oy 3661 CAACGTCTAACTGAGCTTCCAAAGATAAATGATCAAGCGTCTCTTAAAGATGCTTA 3720

```

```

Db 3661 CAACGTCTAACTGAGCTTCCAAAGATAAATGGTACACAGCTCTCTTAAAGATGCCCTTA 3720
Oy 3721 ATCCATTTCTTAGAGACAGACCTTTGTTGAATGATTAACAGAAATGCTGCTGCGCA 3780
Db 3721 ATCCATTTCTTAGAGACAGACCTTTGTTGAATGATTAACAGAAATGCTGCTGCGCA 3780
Oy 3781 GCTGGCTTTCTGCTGAGTGTGACATTAATCAGATTAGGCTGATTTCTCTCACTGAAT 3840
Db 3781 GCTGGCTTTCTGCTGAGTGTGACATTAATCAGATTAGGCTGATTTCTCTCACTGAAT 3840
Oy 3841 TTTGTAATGCTTCCAGACTCTTGGCTGAGAGCGCTGTAGAGATTTCAAGTCCA 3900
Db 3841 TTTGTAATGCTTCCAGACTCTTGGCTGAGAGCGCTGTAGAGATTTCAAGTCCA 3900
Oy 3901 TCATGAAAAATTTGAACACAGAGTGTCTGCTGATGTTTGGGATACGTCATCTT 3960
Db 3901 TCATGAAAAATTTGAACACAGAGTGTCTGCTGATGTTTGGGATACGTCATCTT 3960
Oy 3961 TTAAGGATTTGCTTCATGATTAATTCGAGAGACCTCAACAAAGATCCAGCCTATAC 4020
Db 3961 TTAAGGATTTGCTTCATGATTAATTCGAGAGACCTCAACAAAGATCCAGCCTATAC 4020
Oy 4021 TACATCAGACAAATATGCGCCTGTTCTCTGTGTAAGTATTTGCTTTGG 4080
Db 4021 TACATCAGACAAATATGCGCCTGTTCTCTGTGTAAGTATTTGCTTTGG 4080
Oy 4081 AAACACCCACTGCTTGAATAGCGGTGACAGATGAATGACAGTATACGATCTATAG 4140
Db 4081 AAACACCCACTGCTTGAATAGCGGTGACAGATGAATGACAGTATACGATCTATAG 4140
Oy 4141 TGTTCACAAATTTGAGAAAGTATTTAAATAAACCTGTAAATTTTAACTGACAAATAAA 4200
Db 4141 TGTTCACAAATTTGAGAAAGTATTTAAATAAACCTGTAAATTTTAACTGACAAATAAA 4200
Oy 4201 ATGTTTCTACAGATTAATGTTAACACAGCAAAATTAATGACCCACTTAAAAAAA 4260
Db 4201 ATGTTTCTACAGATTAATGTTAACACAGCAAAATTAATGACCCACTTAAAAAAA 4260
Oy 4261 AAAAAAAA 4268
Db 4261 AAAAAAAA 4268

RESULT 5
HSPFPRBE 3415 bp mRNA linear PRI 23-MAR-1995
LOCUS Human bek mRNA for fibroblast growth factor receptor-BEX.
DEFINITION X52832.1 GI:31373
ACCESSION X52832.1
VERSION 1
KEYWORDS cell surface glycoprotein; fibroblast growth factor receptor; tyrosine kinase.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3415)
AUTHORS Dionne, C.A.
TITLE Direct Substitution
JOURNAL Submitted (01-JUN-1990) Dionne C., Rorer Central Research, 680
Alleluia Road, King of Prussia, PA 19425, USA
2 (bases 1 to 3415)
AUTHORS Dionne, C.A., Crumley, G., Bellot, F., Kaplow, J.M., Searfoss, G.,
Ruta, M., Burgess, W.H., Jaye, M., and Schlessinger, J.
TITLE Cloning and expression of two distinct high-affinity receptors
cross-reacting with acidic and basic fibroblast growth factors
JOURNAL EMBO J. 9 (9), 2685-2692 (1990)
MEDLINE 90360977
PUBMED 1697263
FEATURES
source location/Qualifiers
1..3415
/organism="Homo sapiens"
/db_xref="taxon:9606"
/life_type="draInstem"

```

/clone_lib="lambda gt11"
/dev_stage="neonatal (1 day)"
180..2645
/note="fibroblast growth factor receptor-BEK precursor"

CDS

/codon_start=1
/protein_id="CAA37014.1"
/db_xref="GI:31374"
/translation="MWSMGRICTLVVTAATLSTAPSFVSEDITLLEPEEPTKIOI
SOPEYVAAPGSELEVRCLLKDAVYSMTKIDVHGLPNRRVLIIGYLIQIKATPDS
GLACDASTVSETRYEMVNTDTAISDDDEDIDGADFEVSENSNRKAPVMTTE
KKEKRLHAYPALMAYKFCRPAGNPMPTMRMLKNGKFEQEHIGGYKVRNHSILM
ESVPSDKGNVTCVENEYSINHYHLDVVERSPHPILOAGLPANASTVVGDIEM
YCKVYSDAOPHIQMIKHEKNGSKYGPDLPLYKLKAKAGVNTDKEIEVLIYRNF
EDAGETCLAGNSIGISFHSAMLTVPAPGREKEITASPDYLEIATYCIQVRLINM
VTILCRMKNTRKPKDPSOPAVHKKTRIPLRQVYVAESSSSNSNSTPLVRLITR
LSTADTPMLAYSEVELPEDEPKHEPRRKLTLKGLSGCTGOVVMALAVGIDDKP
KRAVYAVYMKLDDATEKDLSDVSEMEKMTIGKHKNTIILGACTODGPLYVLEY
ASKGNIRELYLRARPPGMEYSYDINKVPEEOMTFDOLVCTQIOLAKMAYLSOKCIH
ROLAARNVLTENNNWKIADFLARDINNIIDYKTKTNGRLPKMMAPEALDRVYTH
OSDVNSFVGLAMEIFTLGSPYGIJVEELFKLKGHRMDLPANTNFIYMMMRDM
HAYPSQRPFKQLEDLDRILTLTNEEYLDLSQPLEOYSPSPYPTDRSSSSGSDSVF
SPDPMPEBCLQIPIHINSVKT"
180..242
519.peptide
mat.peptide
243..2642
/product="mature fibroblast growth factor receptor-BEK"
BASE COUNT 953 a 780 c 865 g 817 t
ORIGIN

Query Match 79.3% Score 3386.6; DB 9; Length 3415;
Best Local Similarity 99.8% Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

93 CACAGTCGCGAGGAGCGCTTGCATTCAAGTACTGACAGCAGCAGCGGCGCTCGG 152
1 CCCAGGTCCGGGAGGCGGTGGCATTCAAGTACTGACAGCAGCAGCGGCGCTCGG 59
153 TTCCTAGCGCCACCGCAGGCTGAAGCATTTGCCGTAGTCCATGCCCGTAGAGAAAGTGT 212
60 TTCCTGAGGCCACCGCA-CCTGAAGCATTTGCCGTAGTCCATGCCCGTAGAGAAAGTGT 118
213 GCAGATGGGATTAAAGCTCACATGGATATGGAAGAGAGACCGGGGATTTGTAACCTAAC 272
119 GCAGATGGGATTAAAGCTCACATGGATATGGAAGAGAGACCGGGGATTTGTAACCTAAC 178
273 CATGTCACGTGGGGTCTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332
179 CATGTCACGTGGGGTCTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
333 GGGCGGCGCTCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
239 GGGCGGCGCTCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
393 CAAATACCAATCTCTCAACAGAGTGTAGTGGCTGCGCGAGGGGAGTCCCTAGAGGT 452
299 CAAATACCAATCTCTCAACAGAGTGTAGTGGCTGCGCGAGGGGAGTCCCTAGAGGT 358
453 GCGCT 512
359 GCGCT 418
513 GCGCAACATAGAGAGTGTATTTGGGAGTGTAGTGGCTGCGCGAGGGGAGTCCCTAGAGGT 572
419 GCGCAACATAGAGAGTGTATTTGGGAGTGTAGTGGCTGCGCGAGGGGAGTCCCTAGAGGT 478
573 AGACTCGGCGCTCTATGCTGTACTGCT 632
479 AGACTCGGCGCTCTATGCTGTACTGCT 538
633 CATGTGTAATGTACAGATGCGCATCTCATCCGAGATGATGAGATGACACCGATGATGTC 692
539 CATGTGTAATGTACAGATGCGCATCTCATCCGAGATGATGAGATGACACCGATGATGTC 598

QY 693 GGAAGATTTTGTCACTGAGAACAGTAACAACAGAGAGACCATTAAGTGAACCAACAGAGA 752
DB 599 GGAAGATTTTGTCACTGAGAACAGTAACAACAGAGAGACCATTAAGTGAACCAACAGAGA 658
QY 753 AAAGATGGAAGAGGGGCTTCATGCTGTGCT 812
DB 659 AAAGATGGAAGAGGGGCTTCATGCTGTGCT 718
QY 813 AGCCGGGGGAGAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAGAGTTTAAAGCA 872
DB 719 AGCCGGGGGAGAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAGAGTTTAAAGCA 778
QY 873 GAGGATTCGATTTGAGAGCTACAAAGTACGAACCAACGACACTGAGGCTCATTAATGGAAG 932
DB 779 GAGGATTCGATTTGAGAGCTACAAAGTACGAACCAACGACACTGAGGCTCATTAATGGAAG 838
QY 933 TGTGTCCTCATCTGCAAGAGGAATTAATACCTGTGAGGAGAAATTAATACGGGTCAT 992
DB 839 TGTGTCCTCATCTGCAAGAGGAATTAATACCTGTGAGGAGAAATTAATACGGGTCAT 898
QY 993 CAATCACGCTACACCTGATGTTGTGAGAGCATGCGCTCACCGGCGCATCTCCCAACG 1052
DB 899 CAATCACGCTACACCTGATGTTGTGAGAGCATGCGCTCACCGGCGCATCTCCCAACG 958
QY 1053 CGGACTCGCGGCAATGCTCCACACTGCTGCGAGAGAGATGAGTTTGTCTGCAAGCT 1112
DB 959 CGGACTCGCGGCAATGCTCCACACTGCTGCGAGAGAGATGAGTTTGTCTGCAAGCT 1018
QY 1113 TTACAGTGTATGCCACCGCCACATCCAGTGTGATCAAGCAGCGTGAAGAAAGAGGCGGTAA 1172
DB 1019 TTACAGTGTATGCCACCGCCACATCCAGTGTGATCAAGCAGCGTGAAGAAAGAGGCGGTAA 1078
QY 1173 ATTAGCGGCGCGAGAGGCTGCTGCTCAAGGTTCTCAAGGCGCGGCTTAAACACAC 1232
DB 1079 ATTAGCGGCGCGAGAGGCTGCTGCTCAAGGTTCTCAAGGCGCGGCTTAAACACAC 1138
QY 1233 GGCAAGAGATTTGAGGCTCTGATTTGGAATGTAATTTGAGGAGGCTGGGGAATA 1292
DB 1139 GGCAAGAGATTTGAGGCTCTGATTTGGAATGTAATTTGAGGAGGCTGGGGAATA 1198
QY 1293 TACGTCTTGGCGGGTAAATTTCTATTGGGATATCTCTTCACTGCTGATGGTTGACAGTTCT 1352
DB 1199 TACGTCTTGGCGGGTAAATTTCTATTGGGATATCTCTTCACTGCTGATGGTTGACAGTTCT 1258
QY 1353 GCCAGGCGCTGGAAGAGAAAGAGATTAAGCTTCCGAGACTACCTTGAGAGATAGCAT 1412
DB 1259 GCCAGGCGCTGGAAGAGAAAGAGATTAAGCTTCCGAGACTACCTTGAGAGATAGCAT 1318
QY 1413 TTACTGATAGGGGCTTCTTAATGCGCTGTATGGGTGAACAGTATCCCTGCGCAAT 1472
DB 1319 TTACTGATAGGGGCTTCTTAATGCGCTGTATGGGTGAACAGTATCCCTGCGCAAT 1378
QY 1473 GAAAGAACAGACCAAGAACCCAGACTTCAGAGCCAGCGGCTGTGACAAAGCTACCAA 1532
DB 1379 GAAAGAACAGACCAAGAACCCAGACTTCAGAGCCAGCGGCTGTGACAAAGCTACCAA 1438
QY 1533 AGCTATCCCGCTGGGAGACAGAGTAAAGTTTGGCTGAGTCACTCTCTCATGAACCTC 1592
DB 1439 AGCTATCCCGCTGGGAGACAGAGTAAAGTTTGGCTGAGTCACTCTCTCATGAACCTC 1498
QY 1593 CAACACCCCGCTGTGAGGATTAACAACAGCGCTCTCTTCAAGGAGAGACCCCATGCT 1652
DB 1499 CAACACCCCGCTGTGAGGATTAACAACAGCGCTCTCTTCAAGGAGAGACCCCATGCT 1558
QY 1653 GGCAGAGGCTCTCGAGTATGAACCTTCCAGAGAGACCCAAATGGAAGTTTCAAGAGATTA 1712
DB 1559 GGCAGAGGCTCTCGAGTATGAACCTTCCAGAGAGACCCAAATGGAAGTTTCAAGAGATTA 1618
QY 1713 GCTGACATGAGGAGCGGCTGGGAGAGGTTGCTTTGGGCAAGGCTGATGCGGGAAGC 1772
DB 1619 GCTGACATGAGGAGCGGCTGGGAGAGGTTGCTTTGGGCAAGGCTGATGCGGGAAGC 1678
QY 1773 AGTGGAAATTGACAAAGAACCCCAAGAGGCGGTACCGTGGCGCTGGAAGATGTTGAA 1832


```

|||||
Db 1679 ACTGGAAATTCACAAAGACCAAGCCCAAGAGAGCGGTCAACCGTGGCGCGGTGAAGATTTTGAA 1738
|||||
Oy 1833 AGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTGCAGAGATGAGATGATCAAGAT 1892
|||||
Db 1739 AGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTGCAGAGATGAGATGATCAAGAT 1798
|||||
Oy 1893 GATTGGGAAACACAGAAATATATATATCTTTGTGAGCCCTGCACACAGAGATGGGCGCT 1952
|||||
Db 1799 GATTGGGAAACACAGAAATATATATCTTTGTGAGCCCTGCACACAGAGATGGGCGCT 1858
|||||
Oy 1953 CATGTGCATAGTTGAGATGCTCTTAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAG 2012
|||||
Db 1859 CATGTGCATAGTTGAGATGCTCTTAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAG 1918
|||||
Oy 2013 GCCACCCGGGATGAGATCTCTATGACATTTAACCGCTTCTCGAGAGACATGACCTT 2072
|||||
Db 1919 GCCACCCGGGATGAGATCTCTATGACATTTAACCGCTTCTCGAGAGACATGACCTT 1978
|||||
Oy 2073 CAAAGCACTTGGTGTATGACCTACCAAGCTGGCCAGAGGCAATGGAGTACTTGGCTTCCCA 2132
|||||
Db 1979 CAAAGCACTTGGTGTATGACCTACCAAGCTGGCCAGAGGCAATGGAGTACTTGGCTTCCCA 2038
|||||
Oy 2133 AAAATGATTCATCGAGATTTAGCACCCAGAAATGTTTTGTAAACAGAAACAAATGTGAT 2192
|||||
Db 2039 AAAATGATTCATCGAGATTTAGCACCCAGAAATGTTTTGTAAACAGAAACAAATGTGAT 2098
|||||
Oy 2193 GAAATATGACAGACTTTGGAGCTGGCCAGACATATCAACAAATATAGACTATTACAAAAAGC 2252
|||||
Db 2099 GAAATATGACAGACTTTGGAGCTGGCCAGACATATCAACAAATATAGACTATTACAAAAAGC 2158
|||||
Oy 2253 CACCATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTTTGATAGATATAT 2312
|||||
Db 2159 CACCATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTTTGATAGATATAT 2218
|||||
Oy 2313 CACTCATCAGAGTATGTCTGTCTCTCGGGGTGTTAATGTGGAGATCTTCACCTTTAGG 2372
|||||
Db 2219 CACTCATCAGAGTATGTCTGTCTCTCGGGGTGTTAATGTGGAGATCTTCACCTTTAGG 2278
|||||
Oy 2373 GGGCTGGCCCTACCCAGAGATTTCCCGTGGAGAACTTTTAAAGCTCTGAGAGAAAGACA 2432
|||||
Db 2279 GGGCTGGCCCTACCCAGAGATTTCCCGTGGAGAACTTTTAAAGCTCTGAGAGAAAGACA 2338
|||||
Oy 2433 CAGAATGATTAAGCCAGCCAACTGACCAACAGAACTGTACATGATGATGAGGACTGTG 2492
|||||
Db 2339 CAGAATGATTAAGCCAGCCAACTGACCAACAGAACTGTACATGATGATGAGGACTGTG 2298
|||||
Oy 2493 GCATGCAAGTCCCTCCAGAGACCAAGCTTCAAGCAAGTGTGAAGACTTGGATGCAAT 2552
|||||
Db 2399 GCATGCAAGTCCCTCCAGAGACCAAGCTTCAAGCAAGTGTGAAGACTTGGATGCAAT 2458
|||||
Oy 2553 TGTACAGCTCAGCAACCAATGAGAAATCTTGGACCTCAGCAACCTCTGCAACAGTATTC 2612
|||||
Db 2459 TGTACAGCTCAGCAACCAATGAGAAATCTTGGACCTCAGCAACCTCTGCAACAGTATTC 2518
|||||
Oy 2613 ACCTAGTTACCTGACACAAAGATTTCTTCTTCAAGAGATGATTTCTTTCTCC 2672
|||||
Db 2519 ACCTAGTTACCTGACACAAAGATTTCTTCTTCAAGAGATGATTTCTTTCTCC 2578
|||||
Oy 2673 AGACCCCATGCTTACCAACCATGCTCTCTCAGTATCCACATATAACGGCAGTGTAA 2732
|||||
Db 2579 AGACCCCATGCTTACCAACCATGCTCTCTCAGTATCCACATATAACGGCAGTGTAA 2638
|||||
Oy 2733 AACATGAATGAGTGTCTGCTGCTGCCAAAGAGACACACTGGGAACTTACCTACAC 2792
|||||
Db 2639 AACATGAATGAGTGTCTGCTGCTGCCAAAGAGACACACTGGGAACTTACCTACAC 2698
|||||
Oy 2793 TGACAGAGGAGACCATCTCTCCAGAGACTTGTCTCTCACTTGTATATATGATCAGAG 2852
|||||
Db 2699 TGACAGAGGAGACCATCTCTCCAGAGACTTGTGTCTCTCACTTGTATATGATCAGAG 2758
|||||
Oy 2853 GAGTAAATTAATTGAAAAAGTATGATATGTGTAAAGATTTATACAGTTGAAAACTTG 2912
|||||

```

```

Db 2759 GAGTAAATTAATTGGAAAAAGTAAATCAGCATATGTGTAAAGATTTATACAGTTGAAACTTG 2818
Oy 2913 TAACTCTCCCGAGAGAGAGAGGATTTCTGAGGACAGTGGACTGGCCGACAGACCCACCATG 2972
Db 2819 TAACTCTCCCGAGAGAGAGAGGATTTCTGAGGACAGTGGACTGGCCGACAGACCCACCATG 2878
Oy 2973 TAACTCTCTCAGCTGCCGCTGCTGCTGAGGACAGTGGACTGGCCGACAGTGGACTGG 3032
Db 2879 TAACTCTCTCAGCTGCCGCTGCTGCTGAGGACAGTGGACTGGCCGACAGTGGACTGG 2938
Oy 3033 GCTTCTGCTCTCTCTGTTAATTTTCTAATTAATGAGAAAGATTTATGTCACACACACTT 3092
Db 2939 GCTTCTGCTCTCTCTGTTAATTTTCTAATTAATGAGAAAGATTTATGTCACACACACTT 2998
Oy 3093 ACAGAGCAAAATGCAATATAGTGTGCTGATGATGATGATTAATATATTAATTAATGAT 3152
Db 2999 ACAGAGCAAAATGCAATATAGTGTGCTGATGATGATGATTAATATATTAATTAATGAT 3058
Oy 3153 AAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3212
Db 3059 AAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3118
Oy 3213 AATGCACTAGAAATTTGCTCTCTCTTTTAAATAGCTATTTGCTAATGCTGTTCTTA 3272
Db 3119 AATGCACTAGAAATTTGCTCTCTCTTTTAAATAGCTATTTGCTAATGCTGTTCTTA 3178
Oy 3273 CACATTAATTTCTTAATTTTACCCAGAGAGTGGAAAAATCTTTCTTTCACAGGAAA 3332
Db 3179 CACATTAATTTCTTAATTTTACCCAGAGAGTGGAAAAATCTTTCTTTCACAGGAAA 3238
Oy 3333 ATGATATAAGCTTAATTTATATATATATATATATATATATATATATATATATATAT 3392
Db 3239 ATGATATAAGCTTAATTTATATATATATATATATATATATATATATATATATATAT 3298
Oy 3393 TTTTCTTCTAATTAATTAAGGAGATTTCTATGAGGACAGACAGAGAGTAAATCTAT 3452
Db 3299 TTTTCTTCTAATTAATTAAGGAGATTTCTATGAGGACAGACAGAGAGTAAATCTAT 3358
Oy 3453 TGGCTTGACCTTAAGTATGATGATCTTTGAAAAAGAAATATTTACATATATATGA 3509
Db 3359 TGGCTTGACCTTAAGTATGATGATCTTTGAAAAAGAAATATTTACATATATATGA 3415

RESULT 6
HSFGFR2UB 3248 bp DNA linear PRI 25-JUN-1997
LOCUS HSFGR2UB
DEFINITION H.sapiens fgfr2 gene (exon 5).
ACCESSION Z69640.1 GI:1200062
VERSION Z69640
KEYWORDS FGFR2 gene; fibroblast growth factor receptor 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3248)
AUTHORS Steinberger,D. and Mueller,U.
TITLE New point mutations in FGFR2 associated with Crouzon Syndrome
JOURNAL Unpublished
REMARK (sites)
REFERENCE 2 (bases 1 to 3248)
AUTHORS Steinberger,D
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1996) Steinberger D., Institute for Human
Genetics, Schlangenzahl 14, Glessen, Germany, 35392
FEATURES
Location/Qualifiers
1..3248
/organism="Homo sapiens"
/isolate="proband 97"
/db_xref="taxon:9606"
/chromosome="10"
/map="q26"
/sex="female"
/tissue_type="blood"

```



```
gene /dev_stage="adult"
      1..3248
exon /gene="figr2"
      1..3248
      /gene="figr2"
      /product="fibroblast growth factor receptor 2"
      /note="exon 1"
      /number=5
variation /gene="figr2"
          /product="fibroblast growth factor receptor 2"
          /note="A(886)->G; Lys(292)->Glu"
          /phenotype="M. Crouzon"
BASE COUNT 915 a 737 c 808 g 788 t
ORIGIN
Query Match 76.0% Score 3244.8; DB 9; Length 3248;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 262 GGTACCGTAACCATGTCAGTGGGGTCTTTCATCTGCTGTCGTGTCACCATGGCA 321
DB 1 GGTACCGTAACCATGTCAGTGGGGTCTTTCATCTGCTGTCGTGTCACCATGGCA 60
QY 322 ACCTTGCCCTGGCCGCCCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 381
DB 61 ACCTTGCCCTGGCCGCCCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 120
QY 382 GAGCACCACCAAAATCAATCTCAACGAGATGAGTGGTGGCCGCGGAG 441
DB 121 GAGCACCACCAAAATCAATCTCAACGAGATGAGTGGTGGCCGCGGAG 180
QY 442 TCGCTAGAGTGGCTGCTGCTTGAAGATGCGCCGCTGATCACTTGAAGATGGG 501
DB 181 TCGCTAGAGTGGCTGCTGCTTGAAGATGCGCCGCTGATCACTTGAAGATGGG 240
QY 502 GTGCACTTGGGGCCCAACATAGAGAGTCTTATTTGGGAGTACTTGCAGTAAAGGC 561
DB 241 GTGCACTTGGGGCCCAACATAGAGAGTCTTATTTGGGAGTACTTGCAGTAAAGGC 300
QY 562 GCCACGCTAGAGACTCGGCTCTATGCTTACTCCAGTAGAGTGTAGACAGTAA 621
DB 301 GCCACGCTAGAGACTCGGCTCTATGCTTACTCCAGTAGAGTGTAGACAGTAA 360
QY 622 ACTTGTACTTCACTGATGTCACAGATGCCATCTCATCGGAGATGAGATGAC 681
DB 361 ACTTGTACTTCACTGATGTCACAGATGCCATCTCATCGGAGATGAGATGAC 420
QY 682 ACCGATGTCGGGAAGTTTGTCAAGTGAAGTAAACAAGAGAGACCATCTG 741
DB 421 ACCGATGTCGGGAAGTTTGTCAAGTGAAGTAAACAAGAGAGACCATCTG 480
QY 742 ACCAACAAGAAAGATGAAAGCGGCTCATGCTGTGCTCGGCAACATCTGCAAG 801
DB 481 ACCAACAAGAAAGATGAAAGCGGCTCATGCTGTGCTCGGCAACATCTGCAAG 540
QY 802 TTTCGCTGGCCAGCGGGGGAACCAATGCAACCATGCGGTGGTGAAGAAAGGGAAG 861
DB 541 TTTCGCTGGCCAGCGGGGGAACCAATGCAACCATGCGGTGGTGAAGAAAGGGAAG 600
QY 862 GAGTTTAAAGAGAGCATGTCATTTGAGAGTACAGATGCAAGAACAGAGACTGAGCTTC 921
DB 601 GAGTTTAAAGAGAGCATGTCATTTGAGAGTACAGATGCAAGAACAGAGACTGAGCTTC 660
QY 922 ATTATGGAAGTGTGCTCCATCTGCAAGGAAATTAATCACTGTGTGTGAGAAATGAA 981
DB 661 ATTATGGAAGTGTGCTCCATCTGCAAGGAAATTAATCACTGTGTGTGAGAAATGAA 720
QY 982 TAGGGTCCATCAATCAAGTACCAACGAGATGTTGTGAGAGTACGCTCAGCGGCC 1041
DB 721 TAGGGTCCATCAATCAAGTACCAACGAGATGTTGTGAGAGTACGCTCAGCGGCC 780
QY 1042 ATCTTCCAAAGCGGAGCTGCGGCAAAATGCCCTCCAGAGTGTGAGAGACGATGATT 1101
```

```
DB 781 ATCTTCCAAAGCGGAGCTGCGGCAAAATGCCCTCCAGAGTGTGAGAGACGATGATT 840
QY 1102 GTCTGCAAGGTTTACAGTATGATGCCAGCCCATCCAGTGTGATCAAGCAGTGAAG 1161
DB 841 GTCTGCAAGGTTTACAGTATGATGCCAGCCCATCCAGTGTGATCAAGCAGTGAAG 900
QY 1162 AACGGCAGTAAATACGGGGCCGAGCGGCTGCTTCACTCAAGGTTTCAAGCGCGCGT 1221
DB 901 AACGGCAGTAAATACGGGGCCGAGCGGCTGCTTCACTCAAGGTTTCAAGCGCGCGT 960
QY 1222 GTTAAACACACGAGCAAGAGATGAGGTTCTCTATTTGGAATGATTAATCTTTGAGAG 1281
DB 961 GTTAAACACACGAGCAAGAGATGAGGTTCTCTATTTGGAATGATTAATCTTTGAGAG 1020
QY 1282 GCTGGGGAATATACGTCCTTGGCGGTAATCTTATTTGGGATATCTTCACTGATGG 1341
DB 1021 GCTGGGGAATATACGTCCTTGGCGGTAATCTTATTTGGGATATCTTCACTGATGG 1080
QY 1342 TTGACAGTTCTGCCAGCGCTGGAGAGAAAGAGATTACAGCTTCCAGACTACCTG 1401
DB 1081 TTGACAGTTCTGCCAGCGCTGGAGAGAAAGAGATTACAGCTTCCAGACTACCTG 1140
QY 1402 GAGATACCATTTACTCATAGGGTCTTCTTAATGCCCTGATGGTGAACAGTATC 1461
DB 1141 GAGATACCATTTACTCATAGGGTCTTCTTAATGCCCTGATGGTGAACAGTATC 1200
QY 1462 CTGTGCCGAATGAAGAACACGACCAAGACAGACTTTCAGAGCCAGCGGCTGTGCAC 1521
DB 1201 CTGTGCCGAATGAAGAACACGACCAAGACAGACTTTCAGAGCCAGCGGCTGTGCAC 1260
QY 1522 AAGCTGACCAAGATATCCCTGCGGAGACAGTAACTTTCGCTGAGTCCAGCTCC 1581
DB 1261 AAGCTGACCAAGATATCCCTGCGGAGACAGTAACTTTCGCTGAGTCCAGCTCC 1320
QY 1582 TCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCCTCTTCAACGGCAGAC 1641
DB 1321 TCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCCTCTTCAACGGCAGAC 1380
QY 1642 ACCGCCATGCTGGCAGAGGCTCTCCAGATGAACTTCCAGAGACCCCAAAATGGAGTTT 1701
DB 1381 ACCGCCATGCTGGCAGAGGCTCTCCAGATGAACTTCCAGAGACCCCAAAATGGAGTTT 1440
QY 1702 CCAAGATTAAGCTGACACCTGGGCAAGCCCTGGGGAAGGTTTGGGCAAGTGTTC 1761
DB 1441 CCAAGATTAAGCTGACACCTGGGCAAGCCCTGGGGAAGGTTTGGGCAAGTGTTC 1500
QY 1762 ATGCGGGAAGCACTGGGAATTGACAAAGAACCCCAAGGAGGCTGCAACCTGGCCGTG 1821
DB 1501 ATGCGGGAAGCACTGGGAATTGACAAAGAACCCCAAGGAGGCTGCAACCTGGCCGTG 1560
QY 1822 AAGATGTGAAGATGATGCGACAGAGAAAGACCTTCTGTGATGTGTGCAGAGATGAG 1881
DB 1561 AAGATGTGAAGATGATGCGACAGAGAAAGACCTTCTGTGATGTGTGCAGAGATGAG 1620
QY 1882 ATGATGAAGATGATGGAAGAACACAGAAATATCAATCTTCTTGGAGCTGTGACAG 1941
DB 1621 ATGATGAAGATGATGGAAGAACACAGAAATATCAATCTTCTTGGAGCTGTGACAG 1680
QY 1942 GATGGCCCTCTATCTCATAGTATGCTTAAAGGCAACCTCCGAGATTAACCTC 2001
DB 1681 GATGGCCCTCTATCTCATAGTATGCTTAAAGGCAACCTCCGAGATTAACCTC 1740
QY 2002 CGAGCCCGGAGGCAACCGGGAATGGTGTCTCTATGAAATTAACCGTCTCTGAGAG 2061
DB 1741 CGAGCCCGGAGGCAACCGGGAATGGTGTCTCTATGAAATTAACCGTCTCTGAGAG 1800
QY 2062 CAGATGACCTTCAAGCACTTGTGTATGACACCTGACAGCTGCGAGAGCAATGAGTAC 2121
DB 1801 CAGATGACCTTCAAGCACTTGTGTATGACACCTGACAGCTGCGAGAGCAATGAGTAC 1860
QY 2122 TTGGCTTCCCAAAATGATTTTATGAGATTTAGACCCAGAAATGTTTGGTAAACAGAA 2181
```

```

Db 1861 TTGGCTTCCCAAAATGTTTCATCGAGATTACAGCCAGAAATGTTTGGTAACAGA 1920
QY 2182 AACCAATGATGATAAAATAGCAGACTTTGGACTGGCCAGAGATATCAACAATATAGACTAT 2241
Db 1921 AACCAATGATGATAAAATAGCAGACTTTGGACTGGCCAGAGATATCAACAATATAGACTAT 1980
QY 2242 TACAAAAAGACCACCAATGGGGGCTTCCAGTCAGTGGATGGCTCCACAAAGCCCTGTTT 2301
Db 1981 TACAAAAAGACCACCAATGGGGGCTTCCAGTCAGTGGATGGCTCCACAAAGCCCTGTTT 2040
QY 2302 GATAGAGTATACACTATCAGATGATGTCTGCTTGGGGTGTAAATGTGGAGATC 2361
Db 2041 GATAGAGTATACACTATCAGATGATGTCTGCTTGGGGTGTAAATGTGGAGATC 2100
QY 2362 TTTCACCTTAAAGGGGCTGGCCCTACCCAGGAGATTCCCGTGGAGAGACTTTTAAAGTCTG 2421
Db 2101 TTTCACCTTAAAGGGGCTGGCCCTACCCAGGAGATTCCCGTGGAGAGACTTTTAAAGTCTG 2160
QY 2422 AAGGAAGACACAGATGATGATTAAGCCAGCCAACTGACCAAGCACTGTATCATGATGATG 2481
Db 2161 AAGGAAGACACAGATGATGATTAAGCCAGCCAACTGACCAAGCACTGTATCATGATGATG 2220
QY 2482 AGGAGACTGTTGGCATGACAGTGGCCCTCCAGAGACCAACGTTCAAGCAGTTGTAGAAAGAC 2541
Db 2221 AGGAGACTGTTGGCATGACAGTGGCCCTCCAGAGACCAACGTTCAAGCAGTTGTAGAAAGAC 2280
QY 2542 TTGGATGCAATTTCTCACTCTCACACCAATGAGCAATACTTGGACCTCAGCCCACTCTC 2601
Db 2281 TTGGATGCAATTTCTCACTCTCACACCAATGAGCAATACTTGGACCTCAGCCCACTCTC 2340
QY 2602 GAACAGATTTACACTGTTAGTTCACGACACAAAGATTTCTTCTTCAGAGATGATTC 2661
Db 2341 GAACAGATTTACACTGTTAGTTCACGACACAAAGATTTCTTCTTCAGAGATGATTC 2400
QY 2662 GTTTTTTCTCCAGACCCCATGCTTACGAACATGCCCTTCAGTATCCACACATTAAC 2721
Db 2401 GTTTTTTCTCCAGACCCCATGCTTACGAACATGCCCTTCAGTATCCACACATTAAC 2460
QY 2722 GGCAGTGTAAACATTAATGACGTGTCTGCCCTGCCCAAGAGACGACGACTGGAA 2781
Db 2461 GGCAGTGTAAACATTAATGACGTGTCTGCCCTGCCCAAGAGACGACGACTGGAA 2520
QY 2782 CCTAGTACACTGACGAGGAGACATGCTCCAGAGACTTGTGTCTCCACTGTATAT 2841
Db 2521 CCTAGTACACTGACGAGGAGACATGCTCCAGAGACTTGTGTCTCCACTGTATAT 2580
QY 2842 ATGATCAGAGGAGTAAATTAATGGAAAGTAAATCAGCATATGTGTAAAGATTTATACAG 2901
Db 2581 ATGATCAGAGGAGTAAATTAATGGAAAGTAAATCAGCATATGTGTAAAGATTTATACAG 2640
QY 2902 TTGAAAACCTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGGACTGCCAC 2961
Db 2641 TTGAAAACCTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGGACTGCCAC 2700
QY 2962 AAGCAGCATGTAACCCCTCTCACTGCGTGTCTTGGCTGGACAGTAGACTCA 3021
Db 2701 AAGCAGCATGTAACCCCTCTCACTGCGTGTCTTGGCTGGACAGTAGACTCA 2760
QY 3022 AGGTGACGTGCGTGTCTTCTGTAAATTTTGTAAATTTGAGAAAGATTTATGTC 3081
Db 2761 AGGTGACGTGCGTGTCTTCTGTAAATTTTGTAAATTTGAGAAAGATTTATGTC 2820
QY 3082 AGCAGACACTTACAGACACAAATGCAATATAGTGTGCGATGATGTAATATATATTC 3141
Db 2821 AGCAGACACTTACAGACACAAATGCAATATAGTGTGCGATGATGTAATATATATTC 2880
QY 3142 AAATTATGATATAATATATATATATATTTTACAGAGATTTTGTATGATTTTAA 3201
Db 2881 AAATTATGATATAATATATATATATATTTTACAGAGATTTTGTATGATTTTAA 2940
QY 3202 ATGATGTGCCAATGACACTTAAGAAATTTGCTCTTTTAAATAGTATTTGGCTAAA 3261
Db 2941 ATGATGTGCCAATGACACTTAAGAAATTTGCTCTTTTAAATAGTATTTGGCTAAA 3000

```

```

QY 3262 TCGTGTCTTACACATTAATTTCTTAATTTTCCACGAGCAGAGTGGAAAAATCTTTC 3321
Db 3001 TCGTGTCTTACACATTAATTTCTTAATTTTCCACGAGCAGAGTGGAAAAATCTTTC 3060
QY 3322 TTTCAGGAAATGATTAACGTTAATTAATTAATTAATTTGTAATTAACAAATTA 3381
Db 3061 TTTCAGGAAATGATTAACGTTAATTAATTAATTAATTTGTAATTAACAAATTA 3120
QY 3382 ATCATTTATAGTTTTTTTTTGTAAATTAAGTGGCAATTTCTATGACGACACAGACT 3441
Db 3121 ATCATTTATAGTTTTTTTTTGTAAATTAAGTGGCAATTTCTATGACGACACAGACT 3180
QY 3442 AGTTTATATGCTTGGACCTTAACAGTATACAGATTCCTTGAAGAAGATATTTTACA 3501
Db 3181 AGTTTATATGCTTGGACCTTAACAGTATACAGATTCCTTGAAGAAGATATTTTACA 3240
QY 3502 ATATATGA 3509
Db 3241 ATATATGA 3248

```

```

RESULT 7
HSEFGR2UA
LOCUS H. sapiens fgfr2 gene. 3248 bp DNA linear PRI 25-JUN-1997
DEFINITION H. sapiens fgfr2 gene.
ACCESSION Z69641.1 GI:1200061
VERSION Z69641.1
KEYWORDS FGFR2 gene; fibroblast growth factor receptor 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 3248)
AUTHORS Steinberger, D., Mulliken, J. and Mueller, U.
TITLE New point mutations in FGFR2 associated with Crouzon Syndrome
REMARK Unpublished
JOURNAL
AUTHORS Steinberger, D.
TITLE Direct Submission
SUBMITTED (20-FEB-1996) Steinberger D., Institute for Human
Genetics, Schlangenzahl 14, Glessen, Germany, 35392
FEATURES
location/Qualifiers
source 1..3248
/organism="Homo sapiens"
/isolate="proband 56"
/db_xref="taxon:9606"
/chromosome="10"
/map="q26"
/sex="Male"
/tissue_type="blood"
/dev_stage="infant"
1..3248
/gene="fgfr2"
1..3248
/exon
/gene="fgfr2"
/product="fibroblast growth factor receptor 2"
/feature="exon U"
/number=5
880

```

```

BASE COUNT 915 a 737 c 808 g 788 t
ORIGIN
Query Match 76.0%; Score 3244.8; DB 9; Length 3248;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 262 GGTACCGTAACATGTCAGCTGGGGTCTTTTCATCTGCTGTGTCGACACATGGCA 321
|||||

```

```

Db      1  GGTACCGTAACCATGTCAGCTGGGGTGTTCATCTGCTGTGTGTGTCACCATGGCA  60
QY      322  ACCTTGTCCCTGGCCGCGCCCTCTCAGTTTATGTGGATACCACATTAAGACCAGAA  381
Db      61  ACCTTGTCCCTGGCCGCGCCCTCTCAGTTTATGTGGATACCACATTAAGACCAGAA  120
QY      382  GAGCCACCAACCAATAACCAATCTCAACACAGAGTGTACGTGGCGCCGAGGAG  441
Db      121  GAGCCACCAACCAATAACCAATCTCAACACAGAGTGTACGTGGCGCCGAGGAG  180
QY      442  TCGGTAGAGGGCGCTGCTGTGAAGATGCCCGCTGATCAGTGGACTAAGATGGG  501
Db      181  TCGGTAGAGGGCGCTGCTGTGAAGATGCCCGCTGATCAGTGGACTAAGATGGG  240
QY      502  GTGCACCTTGGGGCCCAACAATAGACAGTCTTATTTGGGAGTACTTGGCAGTAAGAGGG  561
Db      241  GTGCACCTTGGGGCCCAACAATAGACAGTCTTATTTGGGAGTACTTGGCAGTAAGAGGG  300
QY      562  GCCACGCTAGAGACTCCGGCTCTATGCTTGTACTGCCAGTAGAGACTGTAGACAGTAA  621
Db      301  GCCACGCTAGAGACTCCGGCTCTATGCTTGTACTGCCAGTAGAGACTGTAGACAGTAA  360
QY      622  ACTTGTACTTCAATGATGTACAGATGCCATCTCATCCGAGATGATGAGATGAC  681
Db      361  ACTTGTACTTCAATGATGTACAGATGCCATCTCATCCGAGATGATGAGATGAC  420
QY      682  ACCGATGTGTCGGAGATTTTGTCAGTAGACAGTAAACAAAGAGACCATACTGG  741
Db      421  ACCGATGTGTCGGAGATTTTGTCAGTAGACAGTAAACAAAGAGACCATACTGG  480
QY      742  ACCAACAAGAAAAGATGGAAGCGGCTCATGCTGTGCTCGGCCAACAACACTGTCAAG  801
Db      481  ACCAACAAGAAAAGATGGAAGCGGCTCATGCTGTGCTCGGCCAACAACACTGTCAAG  540
QY      802  TTTTGCCTGCCACCGCGGGGGGAAACCAATGCCAACATCGGCTGTGAAAAACGGGAAG  861
Db      541  TTTTGCCTGCCACCGCGGGGGGAAACCAATGCCAACATCGGCTGTGAAAAACGGGAAG  600
QY      862  GAGTTTAACGAGAGACATGGCATGTGAAGCTACAGAGTACGAAACAGCAGTGGACCTTC  921
Db      601  GAGTTTAACGAGAGACATGGCATGTGAAGCTACAGAGTACGAAACAGCAGTGGACCTTC  660
QY      922  ATTATGGAAGATGTGGTCCCATCTGCACAAGGGAATTAACCTGTGTGTGAGATGAA  981
Db      661  ATTATGGAAGATGTGGTCCCATCTGCACAAGGGAATTAACCTGTGTGTGAGATGAA  720
QY      982  TAGGGTCCATCAATCACACGTACCACTGGATGTTGTGGAGCGATCGCCTCACCGGCC  1041
Db      721  TAGGGTCCATCAATCACACGTACCACTGGATGTTGTGGAGCGATCGCCTCACCGGCC  780
QY      1042  ATCTCTCAAGCCGAGCTCGCGCAAAATGCTCCACAGTGTGGAGAGACCTAGATTT  1101
Db      781  ATCTCTCAAGCCGAGCTCGCGCAAAATGCTCCACAGTGTGGAGAGACCTAGATTT  840
QY      1102  GTCTGCAAGTTTACAGTATGCCAGCCCAATCCAGTGTATAGCAGCTGGAAAAAG  1161
Db      841  GTCTGCAAGTTTACAGTATGCCAGCCCAATCCAGTGTATAGCAGCTGGAAAAAG  900
QY      1162  AAGCGAGTAATAGGGGCGCCGAGCGGCTGCTTACCTCAAGGTTCTCAAGGCCCGCGT  1221
Db      901  AAGCGAGTAATAGGGGCGCCGAGCGGCTGCTTACCTCAAGGTTCTCAAGGCCCGCGT  960
QY      1222  GTTAACACACGAGACAAGAGATTGAGTTCTTATTTGGGAATGTAACTTTGAGAGAC  1281
Db      961  GTTAACACACGAGACAAGAGATTGAGTTCTTATTTGGGAATGTAACTTTGAGAGAC  1020
QY      1282  GCTGGGGAATATACGTGCTTGGCGGGTAATCTATTTGGGATATCTTTCACTTGCATGG  1341
Db      1021  GCTGGGGAATATACGTGCTTGGCGGGTAATCTATTTGGGATATCTTTCACTTGCATGG  1080
QY      1342  TTGACAGTTCGCGCAGCCCTGGGAAGAAAAAGATTAAGCTTCCCGAGACTACTG  1401
Db      1081  TTGACAGTTCGCGCAGCCCTGGGAAGAAAAAGATTAAGCTTCCCGAGACTACTG  1140

QY      1402  GAGATAGCCATTATACGATAGGGGTCTTCTTAATGCCCTGATATGGTGGTAACAGTATC  1461
Db      1141  GAGATAGCCATTATACGATAGGGGTCTTCTTAATGCCCTGATATGGTGGTAACAGTATC  1200
QY      1462  CTGTGCCGAATGGAAGAACAGACCAAGAACCCAGACTTACAGCAGCCAGCCGTGTGAC  1521
Db      1201  CTGTGCCGAATGGAAGAACAGACCAAGAACCCAGACTTACAGCAGCCAGCCGTGTGAC  1260
QY      1522  AACCTGACCAAAAGTATGCCCTGCGGAGACAGTAAAGTTTCCGTGTAGTCCAGCTTC  1581
Db      1261  AACCTGACCAAAAGTATGCCCTGCGGAGACAGTAAAGTTTCCGTGTAGTCCAGCTTC  1320
QY      1582  TCCATGAACTCCAAACACCCCGCTGTGAGGATTAACAACAGCCCTCTTCAACGCGACAC  1641
Db      1321  TCCATGAACTCCAAACACCCCGCTGTGAGGATTAACAACAGCCCTCTTCAACGCGACAC  1380
QY      1642  ACCCCATGCTGGCAGGGGTCTCCGAGTATGAACCTTCCAGAGAGCCCAAAATGGAGTTT  1701
Db      1381  ACCCCATGCTGGCAGGGGTCTCCGAGTATGAACCTTCCAGAGAGCCCAAAATGGAGTTT  1440
QY      1702  CCAAGAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGTTTGTGGCCAAAGTGTTC  1761
Db      1441  CCAAGAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGTTTGTGGCCAAAGTGTTC  1500
QY      1762  ATGGCGGAACGAGTGGGAATTTGACAAAGCAAGCCCAAGAGCGGTCAACCTGGCCGTG  1821
Db      1501  ATGGCGGAACGAGTGGGAATTTGACAAAGCAAGCCCAAGAGCGGTCAACCTGGCCGTG  1560
QY      1822  AAGATTTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTCAAGATGAG  1881
Db      1561  AAGATTTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTCAAGATGAG  1620
QY      1882  ATGATGAAATATTTGGGAACACAAAGATATCATTAATCTTCTTGGAGCCTGCACACAG  1941
Db      1621  ATGATGAAATATTTGGGAACACAAAGATATCATTAATCTTCTTGGAGCCTGCACACAG  1680
QY      1942  GATGGGCCCTCTATGTATGATAGTTGAGTATGCTTAAAGGCAACCTCCAGATACCTC  2001
Db      1681  GATGGGCCCTCTATGTATGATAGTTGAGTATGCTTAAAGGCAACCTCCAGATACCTC  1740
QY      2002  CGAGCCCGGAGGCCACCGGGAGTGGAGTACTCCATGACATTAAACCGTGTCTGGAGG  2061
Db      1741  CGAGCCCGGAGGCCACCGGGAGTGGAGTACTCCATGACATTAAACCGTGTCTGGAGG  1800
QY      2062  CAGATGACCTTCAAGACTTGTGTGATGACACTACAGCTGGCCAGAGGATGGAGTAC  2121
Db      1801  CAGATGACCTTCAAGACTTGTGTGATGACACTACAGCTGGCCAGAGGATGGAGTAC  1860
QY      2122  TTGGCTTCCCAAAAATGATTCATGAGATTTAGAGCCAGAAATGTTTTTGTAAACGAA  2181
Db      1861  TTGGCTTCCCAAAAATGATTCATGAGATTTAGAGCCAGAAATGTTTTTGTAAACGAA  1920
QY      2182  AACAAATGATGAATAATGACAGACTTTGGACTGCCAGAGATATCAACAAATATAGACTAT  2241
Db      1921  AACAAATGATGAATAATGACAGACTTTGGACTGCCAGAGATATCAACAAATATAGACTAT  1980
QY      2242  TACAAAAAGACACCAATGGCGGCTTCCAGTCAAGTGGATGAGCTCCAGAAAGCCTGTT  2301
Db      1981  TACAAAAAGACACCAATGGCGGCTTCCAGTCAAGTGGATGAGCTCCAGAAAGCCTGTT  2040
QY      2302  GATAGAGTATACACTCATCAGAGTATGTCTGTCTTCCGGGGTAAATGTGGAGATC  2361
Db      2041  GATAGAGTATACACTCATCAGAGTATGTCTGTCTTCCGGGGTAAATGTGGAGATC  2100
QY      2362  TTCACTTTAGGGGGCTGGCCTTACCCAGAGATTTCCCTGGAGAACTTTTAAAGCTGCTG  2421
Db      2101  TTCACTTTAGGGGGCTGGCCTTACCCAGAGATTTCCCTGGAGAACTTTTAAAGCTGCTG  2160
QY      2422  AAGGAAGACACAGAAATGAGTAAGCCAGCCAACTGCACCAAGCAAGCTGCATGATCATG  2481
Db      2161  AAGGAAGACACAGAAATGAGTAAGCCAGCCAACTGCACCAAGCAAGCTGCATGATCATG  2220
```


Db 121 GAGCCACCAACCAATACCAATCTCCAAACAGAGTACGTGCTGCACCAAGGGAG 180
Qy 442 TCQCTAGAGTGCCTCCTGTTGAAGATGCGCGCTGCATCTGAGTAAAGATGG 501
Db 181 TCQCTAGAGTGCCTCCTGTTGAAGATGCGCGCTGCATCTGAGTAAAGATGG 240
Qy 502 GTGACTTGGGGCCCAACAATAGAGACGTCTTATTTGGGAGTACTTGCAGATTAAGGGC 561
Db 241 GTGACTTGGGGCCCAACAATAGAGACGTCTTATTTGGGAGTACTTGCAGATTAAGGGC 300
Qy 562 GCCACGCTAGAGACCTCGGCTCTATGCTTGTACTGCTCCGATAGAGATGTAGACATGAA 621
Db 301 GCCACGCTAGAGACCTCGGCTCTATGCTTGTACTGCTCCGATAGAGATGTAGACATGAA 360
Qy 622 ACTTGTACTTCACTGTGTAATGTACAGATGCCATCTCATCCGAGATGATGAGATGAC 681
Db 361 ACTTGTACTTCACTGTGTAATGTACAGATGCCATCTCATCCGAGATGATGAGATGAC 420
Qy 682 ACCGATGGTGGGAATTTTGTCTGAGTACAGATTAACAACAAGAGACCATACTGG 741
Db 421 ACCGATGGTGGGAATTTTGTCTGAGTACAGATTAACAACAAGAGACCATACTGG 480
Qy 742 ACCAACAAGAAAGATGAAAGCGGCTCATGCTGCTGCGGCAACACTGTCAAG 801
Db 481 ACCAACAAGAAAGATGAAAGCGGCTCATGCTGCTGCGGCAACACTGTCAAG 540
Qy 802 TTTTCGCTGCCACCGGGGGGAAACCAATGCCAACCATGGGTGGTGAAGAAAGGGAAG 861
Db 541 TTTTCGCTGCCACCGGGGGGAAACCAATGCCAACCATGGGTGGTGAAGAAAGGGAAG 600
Qy 862 GATTTAAGAGAGATGGCATTTGAGAGGTACAAAGTACGAAACGACAGCTGACCTTC 921
Db 601 GATTTAAGAGAGATGGCATTTGAGAGGTACAAAGTACGAAACGACAGCTGACCTTC 660
Qy 922 ATTATGAAAGTGTGCTCCATCTGACAAAGGAAATTAATACCTGTGGTGAAGATGAA 981
Db 661 ATTATGAAAGTGTGCTCCATCTGACAAAGGAAATTAATACCTGTGGTGAAGATGAA 720
Qy 982 TACGGTCCATCAATACACAGTACACCTGATGTTGTGAGAGCATGCCCTCACGGCCC 1041
Db 721 TACGGTCCATCAATACACAGTACACCTGATGTTGTGAGAGCATGCCCTCACGGCCC 780
Qy 1042 ATCTTCCAAAGCGGAGTGCCTGCGCAATGCTCCACAGTGGTGGAGAGACGTAGAGTT 1101
Db 781 ATCTTCCAAAGCGGAGTGCCTGCGCAATGCTCCACAGTGGTGGAGAGACGTAGAGTT 840
Qy 1102 GTCTGCAAGTTTACAGTATGCCAGCCCAATCCAGTCAAGTCAAGCAGTGAAGAA 1161
Db 841 GTCTGCAAGTTTACAGTATGCCAGCCCAATCCAGTCAAGTCAAGCAGTGAAGAA 900
Qy 1162 AACGCGAATAATAGGGGCGGCGGCAATGCTTACCTCAAGTTCTCAAGCCCGCGGT 1221
Db 901 AACGCGAATAATAGGGGCGGCGGCAATGCTTACCTCAAGTTCTCAAGCCCGCGGT 960
Qy 1222 GTTAAACACCAAGAGATTAAGTGTCTATATTCGGAATGTAACTTTTGGAGAC 1281
Db 961 GTTAAACACCAAGAGATTAAGTGTCTATATTCGGAATGTAACTTTTGGAGAC 1020
Qy 1282 GCTGGGGAATATACGTGCTTGGCGGGTAATTTATTTGGGATATCTTTCACTCTGCATGG 1341
Db 1021 GCTGGGGAATATACGTGCTTGGCGGGTAATTTATTTGGGATATCTTTCACTCTGCATGG 1080
Qy 1342 TTGACAGTTCTCCAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCGACACTACTG 1401
Db 1081 TTGACAGTTCTCCAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCGACACTACTG 1140
Qy 1402 GAGATAGCAATTTACTGATAGGGGTCTTCTTAATCGCTGTATGTTGTAACACTCATC 1461
Db 1141 GAGATAGCAATTTACTGATAGGGGTCTTCTTAATCGCTGTATGTTGTAACACTCATC 1200
Qy 1462 CTGTGCGAATGAAGAAACAGCAAGAGCCAGACTTCAGACGCGGCTGTGCAC 1521
Db 1201 CTGTGCGAATGAAGAAACAGCAAGAGCCAGACTTCAGACGCGGCTGTGCAC 1260

Qy 1522 AAGTCGACCAACGATATCCCTTCGCGAGACAGTAAACGATTTCCGCTGAGTCCAGCTCC 1581
Db 1261 AAGTCGACCAACGATATCCCTTCGCGAGACAGTAAACGATTTCCGCTGAGTCCAGCTCC 1320
Qy 1582 TCCATGAATCCAAACACCCCGGTGTGAGATTAACAACACGCTCTCTTCAACGCGACAC 1641
Db 1321 TCCATGAATCCAAACACCCCGGTGTGAGATTAACAACACGCTCTCTTCAACGCGACAC 1380
Qy 1642 ACCCCATGCTGCGAGGGGTCTCCGATATGAACCTTCAGAGAGACCCAAATGGAGTTT 1701
Db 1381 ACCCCATGCTGCGAGGGGTCTCCGATATGAACCTTCAGAGAGACCCAAATGGAGTTT 1440
Qy 1702 CCAAGATTAAGTGAACACTGCGGCAAGCCCTGCGGAAAGTTGCTTTGGGCAAGTGTC 1761
Db 1441 CCAAGATTAAGTGAACACTGCGGCAAGCCCTGCGGAAAGTTGCTTTGGGCAAGTGTC 1500
Qy 1762 ATGCGGAAGCAGTGGGAATTTGACAAAGAACCCCAAGAGGGGTCCACGGTGGCGCTG 1821
Db 1501 ATGCGGAAGCAGTGGGAATTTGACAAAGAACCCCAAGAGGGGTCCACGGTGGCGCTG 1560
Qy 1822 AAGATTTGAAGATGATGCCACAGAGAAACCTTCTGATCTGGTGTACAGATGAG 1881
Db 1561 AAGATTTGAAGATGATGCCACAGAGAAACCTTCTGATCTGGTGTACAGATGAG 1620
Qy 1882 ATGATGAATGATTTGGGAAACACAGAAATATCATTAATCTTCTTGGAGCTGCACACAG 1941
Db 1621 ATGATGAATGATTTGGGAAACACAGAAATATCATTAATCTTCTTGGAGCTGCACACAG 1680
Qy 1942 GATGGCCCTCTATGCTATGATTTGATGATGCTCTTAAAGGCACTCCGACAAATACCTC 2001
Db 1681 GATGGCCCTCTATGCTATGATTTGATGATGCTCTTAAAGGCACTCCGACAAATACCTC 1740
Qy 2002 CGAGCCCGGAGGCGACCCCGGATGAGATGCTCTATGACATTAACCGTTCTCAGAG 2061
Db 1741 CGAGCCCGGAGGCGACCCCGGATGAGATGCTCTATGACATTAACCGTTCTCAGAG 1800
Qy 2062 CAGATGACCTTGAAGACTTGGTGTATGACACCTACCGAGCTGGCGAGAGCATGAGTAC 2121
Db 1801 CAGATGACCTTGAAGACTTGGTGTATGACACCTACCGAGCTGGCGAGAGCATGAGTAC 1860
Qy 2122 TTGGCTTCCCAAAATGTAATTCATGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAA 2181
Db 1861 TTGGCTTCCCAAAATGTAATTCATGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAA 1920
Qy 2182 AACCAATGATGAATAATGACACTTTGGACTCGCCAGAGATATTAACAATATAGACTAT 2241
Db 1921 AACCAATGATGAATAATGACACTTTGGACTCGCCAGAGATATTAACAATATAGACTAT 1980
Qy 2242 TACAAAAAGACCAACCAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAAGCCGTGTT 2301
Db 1981 TACAAAAAGACCAACCAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAAGCCGTGTT 2040
Qy 2302 GATTAAGTATACACTATCAGAGTATGTCTGTGCTCTTGGGGGTATTAATGTGGAGATC 2361
Db 2041 GATTAAGTATACACTATCAGAGTATGTCTGTGCTCTTGGGGGTATTAATGTGGAGATC 2100
Qy 2362 TTCACTTTAGGGGGCTGCCCTTACCAGAGGATCCCGTGGAGAACTTTTAACTGTGTG 2421
Db 2101 TTCACTTTAGGGGGCTGCCCTTACCAGAGGATTTCCCGTGGAGAACTTTTAACTGTGTG 2160
Qy 2422 AAGGAAGACACAGATGATTAAGCCAGCCAACTGACCAAGAACTTACATGATGATG 2481
Db 2161 AAGGAAGACACAGATGATTAAGCCAGCCAACTGACCAAGAACTTACATGATGATG 2220
Qy 2482 AAGGACTTGGGAGTGCAGTGCCTCCAGAGACCAACGTTTCAAGAGTGGTGAAGAC 2541
Db 2221 AAGGACTTGGGAGTGCAGTGCCTCCAGAGACCAACGTTTCAAGAGTGGTGAAGAC 2280
Qy 2542 TTGATGCAATTTCTACACTCTCAACAACCAATGAGCAATCTTGGAGCTGACGCAACTCTC 2601
Db 2281 TTGATGCAATTTCTACACTCTCAACAACCAATGAGCAATCTTGGAGCTGACGCAACTCTC 2340


```
Db 506 GATACCAATTAAGACCCAGAAAGCCACCAACCAATACCAATCTCTCAACCCAGAAAGTG 565
Qy 421 TAGGCGCTGCGCAGGAGGAGTGCCTAGAGTGGCGCTGCTGTGAAGATGCGCCGTG 480
    |||||
Db 566 TAGTGGCTGCGCAGGAGGAGTGCCTAGAGTGGCGCTGCTGTGAAGATGCGCCGTG 625
Qy 481 ATGAGTTGGACTAAGAGTGGGTGCACATTGGGGCCCAACAATAGAGACAGTCTTATTTGG 540
    |||||
Db 626 ATCAGTTGGACTAAGAGTGGGTGCACATTGGGGCCCAACAATAGAGACAGTCTTATTTGG 685
Qy 541 GACTACTTGGAGTAAGAGGCGCCAGCGCTAGAGACTCCGCGCTCTATGCTTGTACTGCC 600
    |||||
Db 686 GACTACTTGGAGTAAGAGGCGCCAGCGCTAGAGACTCCGCGCTCTATGCTTGTACTGCC 745
Qy 601 AGTAGAGCTGTAGACAGTAAACTGTGTACTTGCATGTGAATGTCAAGATGCAATCTCA 660
    |||||
Db 746 AGTAGAGCTGTAGACAGTAAACTGTGTACTTGCATGTGAATGTCAAGATGCAATCTCA 805
Qy 661 TCCGGAGATGATGAGATGACACCGATGCTGCGGAAGATTTTGTCAGTAGAGACATGAC 720
    |||||
Db 806 TCCGGAGATGATGAGATGACACCGATGCTGCGGAAGATTTTGTCAGTAGAGACATGAC 865
Qy 721 AACAAAGAGACACCACTACTGAGCCACACAGAAAGATGGAAGAGCGCTCCATGCTGTG 780
    |||||
Db 866 AACAAAGAGACACCACTACTGAGCCACACAGAAAGATGGAAGAGCGCTCCATGCTGTG 925
Qy 781 CCTGCGGCCACACTGTCAAGTTTGCCTGCCAGCGGGGGGAACCCATATGCCAATCATG 840
    |||||
Db 926 CCTGCGGCCACACTGTCAAGTTTGCCTGCCAGCGGGGGGAACCCATATGCCAATCATG 985
Qy 841 CGGTGGCTGAAAAAGCGGAAGAGTTTAAGCAGAGACATGCGATTGGAGGCTTACAAAGTA 900
    |||||
Db 986 CGGTGGCTGAAAAAGCGGAAGAGTTTAAGCAGAGACATGCGATTGGAGGCTTACAAAGTA 1045
Qy 901 CGAAACCAAGCACTGAGCCCTCATTTAGAAAGTGTGTCCATCTGACAGAGGAATTTT 960
    |||||
Db 1046 CGAAACCAAGCACTGAGCCCTCATTTAGAAAGTGTGTCCATCTGACAGAGGAATTTT 1105
Qy 961 ACCTGTGTGTGGAGAAATGATACGGGTCCATCAATTCACACGTACACCTGTGATTTGTG 1020
    |||||
Db 1106 ACCTGTGTGTGGAGAAATGATACGGGTCCATCAATTCACACGTACACCTGTGATTTGTG 1165
Qy 1021 GAGCATGCGCTCACCGGCCATCTCCCAAGCCGGAGTGGCGGCAATATGCCCTCCACAGTG 1080
    |||||
Db 1166 GAGCATGCGCTCACCGGCCATCTCCCAAGCCGGAGTGGCGGCAATATGCCCTCCACAGTG 1225
Qy 1081 GTGCGAGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGTATGCCAGCCCAATCCAG 1140
    |||||
Db 1226 GTGCGAGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGTATGCCAGCCCAATCCAG 1285
Qy 1141 TGGATCAAGACGTGTGAAAAAAGACGGGAGTAAATACGGGCCCGACGGCTGCTCACTTC 1200
    |||||
Db 1286 TGGATCAAGACGTGTGAAAAAAGACGGGAGTAAATACGGGCCCGACGGCTGCTCACTTC 1345
Qy 1201 AAGGTTTCAAGGCGCGCGGTGTAAACACACGACGACAAAGAGATGAGTGTCTCTAATTT 1260
    |||||
Db 1346 AAGGTTTCAAGGCGCGGTGTAAACACACGACGACAAAGAGATGAGTGTCTCTAATTT 1400
Qy 1261 CGGAATGTAACCTTTTGAAGACGCTGGGGAATATACGTCCTTGGCGGGTAAATTTATTTGG 1320
    |||||
Db 1401 -TCAATGTGACGAGGCGGATCTGGGGAATATATGTAAAGTGTCCAAATTTATATAGGG 1459
Qy 1321 ATATCCCTTCACTGCTGATGGTGTGACAGTGTGCC-----AGGCGCTGGAAGAGAA 1371
    |||||
Db 1460 CAGGCAACCAAGTGTGCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1519
Qy 1372 AAGAGATTAACAGCTTCCCGACACTACCTGAGATAGCCATTTACTGATAGGGGTCTTC 1431
    |||||
Db 1520 AAGAGATTAACAGCTTCCCGACACTACCTGAGATAGCCATTTACTGATAGGGGTCTTC 1579
Qy 1432 TTAAATCGGCTGTATGTGTGTAAAGTCACTCTGTGTGCGGAATGAAGACAGACCAAGAG 1491
    |||||
Db 1580 TTAAATCGGCTGTATGTGTGTAAAGTCACTCTGTGTGCGGAATGAAGACAGACCAAGAG 1639
    |||||

Qy 1492 CCAGACTTACGACGCGCGGCTGTGCACAAAGCTGACCAAAAGTATWCCCGCTGCGGAGA 1551
    |||||
Db 1640 CCAGACTTACGACGCGCGGCTGTGCACAAAGCTGACCAAAAGTATWCCCGCTGCGGAGA 1699
Qy 1552 CAGGTAAAGTTTCCGCTGATGTCACAGTCTCTGATGATGATCCAAACCCCGCTGTGAGG 1611
    |||||
Db 1700 CAGGTAAAGTTTCCGCTGATGTCACAGTCTCTGATGATGATCCAAACCCCGCTGTGAGG 1759
Qy 1612 ATAAACAACGCGCTCTCTTCAACGAGAGACACCCCATGCTGGAGGGGTCCGAGAT 1671
    |||||
Db 1760 ATAAACAACGCGCTCTCTTCAACGAGAGACACCCCATGCTGGAGGGGTCCGAGAT 1819
Qy 1672 GAACCTTCCAGAGAGCCCAAAATGAGATTGCCAAGAGATTAACCTGACACTGGCAAGCC 1731
    |||||
Db 1820 GAACCTTCCAGAGAGCCCAAAATGAGATTGCCAAGAGATTAACCTGACACTGGCAAGCC 1879
Qy 1732 CTGGGAAGGTTTGGCTTGGGCAATGGTCAATGGCGGAAGCAGTGGGAATTGACAAAGAC 1791
    |||||
Db 1880 CTGGGAAGGTTTGGCTTGGGCAATGGTCAATGGCGGAAGCAGTGGGAATTGACAAAGAC 1939
Qy 1792 AAGCCCAAGAGGCGGTCACCGTGGCCGCTGAAGATGTTGAAAGATGATGCCACAGAAA 1851
    |||||
Db 1940 AAGCCCAAGAGGCGGTCACCGTGGCCGCTGAAGATGTTGAAAGATGATGCCACAGAAA 1999
Qy 1852 GACCTTTCTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGAAACACAAAGAT 1911
    |||||
Db 2000 GACCTTTCTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGAAACACAAAGAT 2059
Qy 1912 ATCATAAATCTTCTTGTGAGCCGTGCACACAGATGAGGCGCTCTATATGTATGTAGAT 1971
    |||||
Db 2060 ATCATAAATCTTCTTGTGAGCCGTGCACACAGATGAGGCGCTCTATATGTATGTAGAT 2119
Qy 1972 GCCTTAAAGGCAACCTCCGAGAAATACCTCGAGCCGCGAGGCCACCGGATGAGATAC 2031
    |||||
Db 2120 GCCTTAAAGGCAACCTCCGAGAAATACCTCGAGCCGCGAGGCCACCGGATGAGATAC 2179
Qy 2032 TCCATGACATTTAACCGTGTCTGTGAGAGAGATGAGTGTGACCTTCAAGAGATTTGTGTATGC 2091
    |||||
Db 2180 TCCATGACATTTAACCGTGTCTGTGAGAGAGATGAGTGTGACCTTCAAGAGATTTGTGTATGC 2239
Qy 2092 ACCTAACAGCTGGCCAGAGGAGTGAATGCTTGTGCTCCCAAAATGATTTATTCAGAGAT 2151
    |||||
Db 2240 ACCTAACAGCTGGCCAGAGGAGTGAATGCTTGTGCTCCCAAAATGATTTATTCAGAGAT 2299
Qy 2152 TTAGAGCCAGAAATGTTTGTGTAAACAGAAACAAATGTGATGAAATATGACAGACTTTGGA 2211
    |||||
Db 2300 TTAGAGCCAGAAATGTTTGTGTAAACAGAAACAAATGTGATGAAATATGACAGACTTTGGA 2359
Qy 2212 CTGCGCAAGATATCAACAAATATGACTATTTACAAAAAGACCAACCAATGGGCGGCTTCCA 2271
    |||||
Db 2360 CTGCGCAAGATATCAACAAATATGACTATTTACAAAAAGACCAACCAATGGGCGGCTTCCA 2419
Qy 2272 GTCAATGATGAGTCCAGAAAGCCCTGTTTGTATAGAGTATACACTCATCAGAGTGTGTC 2331
    |||||
Db 2420 GTCAATGATGAGTCCAGAAAGCCCTGTTTGTATAGAGTATACACTCATCAGAGTGTGTC 2479
Qy 2332 TGGTCCCTTCCGCGGTTTAAATGTGGAGATCTTCACTTTAAGGGGCTGCGCTACCCAGGG 2391
    |||||
Db 2480 TGGTCCCTTCCGCGGTTTAAATGTGGAGATCTTCACTTTAAGGGGCTGCGCTACCCAGGG 2539
Qy 2392 ATTCGCGTGAAGAACTTTTAAAGCTGCTGAAGAGAGACACAAATGATTAACCGAGCC 2451
    |||||
Db 2540 ATTCGCGTGAAGAACTTTTAAAGCTGCTGAAGAGAGACACAAATGATTAACCGAGCC 2599
Qy 2452 AACTGCACCAAGCAAGTGTACATATGATGAGGACGTGTGGCATGTCGATGCGCTCCAG 2511
    |||||
Db 2600 AACTGCACCAAGCAAGTGTACATATGATGAGGACGTGTGGCATGTCGATGCGCTCCAG 2659
Qy 2512 AGACCAAGCTTCAAGCAAGTGTGTGAAGACTTGTGATGGAATTTCTACATTCACAAACCAAT 2571
    |||||
Db 2660 AGACCAAGCTTCAAGCAAGTGTGTGAAGACTTGTGATGGAATTTCTACATTCACAAACCAAT 2719
    |||||
```


QY	1321	ATATCTCTTCACTCTGCATGSGTTGCACAGTTCTGCCAGCGCCTGGAAAGAAAGAGATTT	1380
Db	1427	-----	1428
QY	1381	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTACTGATAGGGGCTTCTTAATGCC	1440
Db	1427	-----	1426
QY	1441	TGTATGCTGGTAACAGTCACTCTGTGCCGAATGAAGAACACGACCAAGACCAGACTTC	1500
Db	1427	-----	1426
QY	1501	AGCAGCCAGCGCGTGTGCACAAAGCTGACCAAAAGTATCCCCCTGGGAGACAGTAA	1560
Db	1427	-----	1426
QY	1561	GTTTCGGCTGAGTCCAGCTCCTCCATGAGTCCAAACACCCGCTGTGAGGATAAACA	1620
Db	1427	GTTCGGCTGAGTCCAGCTCCTCCATGAGTCCAAACACCCGCTGTGAGGATAAACA	1486
QY	1621	CGCCTCTTCAACGGCAGACCCCCCATGCTGGCAGGGTCTCCAGTATGAACCTTCA	1680
Db	1487	CGCCTCTTCAACGGCAGACCCCCCATGCTGGCAGGGTCTCCAGTATGAACCTTCA	1546
QY	1681	GAGGACCCAAATGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAA	1740
Db	1547	GAGGACCCAAATGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAA	1606
QY	1741	GGTTGCTTTGGGCAAGTGGTCAATGGGGAAGCAGTGGGAATTGACAAAGACCAAGCCCA	1800
Db	1607	GGTTGCTTTGGGCAAGTGGTCAATGGGGAAGCAGTGGGAATTGACAAAGACCAAGCCCA	1666
QY	1801	GAGCGGCTACCGTGGCCGCTGAAGATGTTGAAGATGATCCACAGAGAAAGACCTTTC	1860
Db	1667	GAGCGGCTACCGTGGCCGCTGAAGATGTTGAAGATGATCCACAGAGAAAGACCTTTC	1726
QY	1861	GATCTGGTGCACAGATGGAGATGATGAGATGATTTGGAAACACAAAGATTCATTAAT	1920
Db	1727	GATCTGGTGCACAGATGGAGATGATGAGATGATTTGGAAACACAAAGATTCATTAAT	1786
QY	1921	CTTCTTGGAGCTGCACACAGATGGGCGCTCTATGTCATCTAGTATGCTCTATAA	1980
Db	1787	CTTCTTGGAGCTGCACACAGATGGGCGCTCTATGTCATCTAGTATGCTCTATAA	1846
QY	1981	GGGAACTCCGAGAAATCTCCGAGCCCCGGAGGCCAACCCGGGATGAGTACTCTATGAC	2040
Db	1847	GGGAACTCCGAGAAATCTCCGAGCCCCGGAGGCCAACCCGGGATGAGTACTCTATGAC	1906
QY	2041	ATTAACTGTTCTCTGAGGAGCAGATGATGATCTTCAAGGACTGGTGTGATGCACTACAG	2100
Db	1907	ATTAACTGTTCTCTGAGGAGCAGATGATGATCTTCAAGGACTGGTGTGATGCACTACAG	1966
QY	2101	CTGGCCAGAGGCATGAGTACTTGGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCC	2160
Db	1967	CTGGCCAGAGGCATGAGTACTTGGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCC	2026
QY	2161	ACAAATGTTTGGTAAACAAAAACAATGATGAAGAAATGCGAGACTTGTGACTCGCCACA	2220
Db	2027	ACAAATGTTTGGTAAACAAAAACAATGATGAAGAAATGCGAGACTTGTGACTCGCCACA	2086
QY	2221	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	2280
Db	2087	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	2146
QY	2281	ATGGCTCCAGGAAGCCCTGTTGATGAGATATACACTCATCAAGTATGTCGTGCTTTC	2340
Db	2147	ATGGCTCCAGGAAGCCCTGTTGATGAGATATACACTCATCAAGTATGTCGTGCTTTC	2206
QY	2341	GGGGTGTAAATGTGGAGATCTTCACTTTAGGGGCTCGCCTTACCAGAGATTCGCCGG	2400
Db	2207	GGGGTGTAAATGTGGAGATCTTCACTTTAGGGGCTCGCCTTACCAGAGATTCGCCGG	2266
QY	2401	GAGGAACTTTTTAACTCTCTGAAGAGACACAAATGATTAAGCCAGCCAACTGCACC	2460

Db	2267	GAGGAACTTTTAAAGCTGCTCAGAGAGGACACAGAAATGGATTAAGCCAGCCAACTGCACC	2326
Qy	2461	AACGAACCTGACATGATGATGAGGAGACTGTGGCATGCGAGGCCCTCCAGACCAAG	2520
Db	2327	AACGAACCTGACATGATGATGATGAGGAGACTGTGGCATGCGAGGCCCTCCAGACCAAG	2366
Qy	2521	TTCAAGAGCTGGTGAAGAACTTTGAGTTCGAATTTCTCACTCTCACACCAATGAGAAATAC	2560
Db	2387	TTCAAGAGAGTTGGTAGAAGACTTTGGATTCGAATTTCTCACTCTCACACCAATGAGAAATAC	2446
Qy	2581	TTGAGACCTCAGCCAACTCTCAGAACAGTATTCACCTAGTTACCTTGACACAAAGAGTCT	2640
Db	2447	TTGAGACCTCAGCCAACTCTCAGAACAGTATTCACCTAGTTACCTTGACACAAAGAGTCT	2506
Qy	2641	TGTTCTTCAGAGAGATGATTCGTTTTTTCACAGACCCCATGCGCTTACGAACCATGCTT	2700
Db	2507	TGTTCTTCAGAGAGATGATTCGTTTTTTCACAGACCCCATGCGCTTACGAACCATGCTT	2566
Qy	2701	CCTCAGATATCCACATATAAAGGAGGATTAACATGAAATGACTGTGTGCTGTGCTCC	2760
Db	2567	CCTCAGATATCCACATATAAAGGAGGATTAACATGAAATGACTGTGTGCTGTGCTCC	2626
Qy	2761	CAACAGAGACAGCACTGGGAACCTAGCTACACTGAGCAGAGAGACCATGCTCCAGAGC	2820
Db	2627	CAACAGAGACAGCACTGGGAACCTAGCTACACTGAGCAGAGAGACCATGCTCCAGAGC	2686
Qy	2821	TTGTGTCTCCACTCTGTATATATGATCAGAGAGTAAATATTTGAAAAAGTAATCAGCA	2880
Db	2687	TTGTGTCTCCACTCTGTATATATGATCAGAGAGTAAATATTTGAAAAAGTAATCAGCA	2746
Qy	2881	TATGTGTAAAGATTTATACAGTTGAAACCTGTAACTTCCCGAGGAGGAAGAGTT	2940
Db	2747	TATGTGTAAAGATTTATACAGTTGAAACCTGTAACTTCCCGAGGAGGAAGAGTT	2806
Qy	2941	TCGAGAGCAATGCACATGCCACCAAGCCACCATGTAAACCCCTCTGACCTGCCGTCTCTG	3000
Db	2807	TCGAGAGCAATGCACATGCCACCAAGCCACCATGTAAACCCCTCTGACCTGCCGTCTCTG	2866
Qy	3001	GCTGTGAGCAGTAAAGAGACTCAAGGTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	3060
Db	2867	GCTGTGAGCAGTAAAGAGACTCAAGGTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	2926
Qy	3061	TAAATGGAGAGATTTATATGTCAGCACACACTTACAGAGCAAAATGCAGATATATAGTGC	3120
Db	2927	TAAATGGAGAGATTTATATGTCAGCACACACTTACAGAGCAAAATGCAGATATATAGTGC	2986
Qy	3121	TGATGTATGTAAATATATTCAAAT	3180
Db	2987	TGATGTATGTAAATATATTCAAAT	3046
Qy	3181	TATTTTGTATATGATTTTAAATGATGTGCCAATGCACCTACCTAGAAAATTTGGTCTCTT	3240
Db	3047	TATTTTGTATATGATTTTAAATGATGTGCCAATGCACCTACCTAGAAAATTTGGTCTCTT	3106
Qy	3241	TTTTATATACCTATTTTCTTAAATGCTGTCTTACACATTAATTTCTTATATTTTACCGAGCA	3300
Db	3107	TTTTATATACCTATTTTCTTAAATGCTGTCTTACACATTAATTTCTTATATTTTACCGAGCA	3166
Qy	3301	GAGGTGGAAAAATACTTTGCTTTCAGGAAAAATGGTATATACGTTAATTTAATTAATTAAT	3360
Db	3167	GAGGTGGAAAAATACTTTGCTTTCAGGAAAAATGGTATATACGTTAATTTAATTAATTAAT	3226
Qy	3361	TGGTATATATACAAAAACA 3378	
Db	3227	TGGTATATATACAAAAACA 3244	

ACCESSION	M87771
VERSION	M87771.1 GI:186781
KEYWORDS	K-sam-III; fibroblast growth factor receptor.
SOURCE	Homo sapiens cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hemo. 1 (bases 1 to 3244)
AUTHORS	Katoh,M., Hattori,Y., Sasaki,H., Tanaka,M., Sugano,K., Yazaki,Y., Sugimura,T. and Terada,M. K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 89 (7), 2960-2964 (1992)
PUBMED	92212948
FEATURES	1313574
SOURCE	location/Qualifiers
	1..3244
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/cell_line="NOC-IT"
	1..3244
gene	/gene="K-sam-III"
	488..2605
CDS	/gene="K-sam-III"
	/codon_start=1
	/product="Fibroblast growth factor receptor"
	/protein_id="AAA59471.1"
	/db_xref="GI:186782"
	/translation="MVSMGRFCICLVVVTMTLSARPSFLVEDTTLPEEPPTKYOI SOPHYVAAPGESLEVRCLIKDAVISMTKGVLGNNRVLTGEYLOKAGPRDS GLACTASRTYDSETFYFMVYTDAISGDEDDTDCAEDVSNSNNRAPWTNE EMERELHVAIPANTVKFRCPAGGPMPLMRLLKNGKEFKOHRIGCYKRQHSILIM ESKVDSCGNATCVENEYGSINHTIHLDVERSPHPRLDAGLPAAASTVGSDVEE LCKAYSDAOPHIQWIKHEKSGSYGGDLPLYKLVAASSSSNMSNPVLNTRR VSTADTPMLAGVEYELEPDKPKWEFPDRDKLTLLKPLGEGECGVNAAEVGDIDKP KEATVAVAKMLKDATERKOLDSLSEMEMMIKKNIILILACRGDELYIVLEY ASKGULREYLARRPPGMGYSDIINRYMEBOMETKDLVSCYOLARGMEVLAOSCIIE RDLAARNLYLVENNYFTLKADRCALRDINNIDYKKTNGRLPVKWWAPELLFDVYTH HADVSRFGVMKEIFTLGCGSPGPIPYBELKLKLBGRMKRPANCNINELMYMRDCM OASVWSRPTFEQLVEDDRIILLTTTNBEERYLDLSOLFYSYFDTRSCESSGDSVF SPDPPEYPEDCLPYPHINGSVKT"
	488..550
sig_peptide	/gene="K-sam-III"
BASE COUNT	861 a 795 c 852 g 736 t
ORIGIN	
Query Match	62.6%; Score 2670.4; DB 9; Length 3244;
Best Local Similarity	89.7%; Pred. No. 0;
Matches 3029; Conservative	0; Mismatches 1; Indels 348; Gaps 1;
Oy	1 CCCAAGACCACCTTCCTCCTGTGGAGTGTGCCTCCACACACCCGGCGCTGCTTC 60
Db	215 CCCAAGACCACCTTCCTCCTGTGGAGTGTGCCTCCACACACCCGGCGCTGCTTC 274
Oy	61 TCCATCCGACCCACGCCGGGGCGCGGGACAACACAGTGCGGGAGAAGCGTTGCCATT 120
Db	275 TCCATCCGACCCACGCCGGGGCGCGGGACAACACAGTGCGGGAGAAGCGTTGCCATT 334
Oy	121 AACTGACTGCAGCAGCAGCGGGCGACGCCCTTCGTTCTTAGCCCCACCGCACGCTGAAGGA 180
Db	335 AACTGACTGCAGCAGCAGCGGGCGACGCCCTTCGTTCTTAGCCCCACCGCACGCTGAAGGA 394
Oy	181 TTCGGGTAAGTCCATGCCCCTAGAGAAAGTGCACATGGATGGAATTAACTGCACATGGAGA 240
Db	395 TTCGGGTAAGTCCATGCCCCTAGAGAAAGTGCACATGGATGGAATTAACTGCACATGGAGA 454
Oy	241 TATGGAAGAGACCGGGGATTTGGTACCGTAACCATGCTAGCTGGGCTGTTTCATCTGC 300
Db	455 TATGGAAGAGACCGGGGATTTGGTACCGTAACCATGCTAGCTGGGCTGTTTCATCTGC 514
Oy	301 CTGTGCTGTGTACACATGCCAACCTTGTCCCTGGCCCGGCCCTTCAGTTAGTTAGTGA 360
Db	515 CTGTGCTGTGTACACATGCCAACCTTGTCCCTGGCCCGGCCCTTCAGTTAGTTAGTGA 574

Oy	361	CATACCACATTAGACCCAGAAAGAGCCACCAACCAAAATGCTCAGCAACAAAGG	420
Oy	362	CATACCACATTAGACCCAGAAAGAGCCACCAACCAAAATGCTCAGCAACAAAGG	420
Db	575	GATTACCACATTAGACCCAGAAAGAGCCACCAACCAAAATGCTCAGCAACAAAGG	634
Oy	421	TACGTGGCTGCCCGCAGGGGAGTCCGTAGAGGTGCGCTGCTGTTGAAGATGCCCGCTG	480
Db	635	TACGTGGCTGCCCGCAGGGGAGTCCGTAGAGGTGCGCTGCTGTTGAAGATGCCCGCTG	694
Oy	481	ATCAGTTGACATTAGAGATGGGGTGCACATTGGGGCCCAACATATAGACAGTGTATTGGG	540
Db	695	ATCAGTTGACATTAGAGATGGGGTGCACATTGGGGCCCAACATATAGACAGTGTATTGGG	754
Oy	541	GAGTACTTGCATTAAGAGGGCGCCACAGCCCTAAGACTCCGGCCTGTATGCTTGTACTGCC	600
Db	755	GAGTACTTGCATTAAGAGGGCGCCACAGCCCTAAGACTCCGGCCTGTATGCTTGTACTGCC	814
Oy	601	AGTAGACTGTAGACAGTAGAATCTTGTAATCTTCATATGTGTAATGTCAAGATGCCATCTCA	660
Db	815	AGTAGACTGTAGACAGTAGAATCTTGTAATCTTCATATGTGTAATGTCAAGATGCCATCTCA	874
Oy	661	TCCGGGATGATAGAGATGACACCCGATGGTGGCGGAAGATTTTGTGCTAGTAGAAGAGTAAC	720
Db	875	TCCGGGATGATAGAGATGACACCCGATGGTGGCGGAAGATTTTGTGCTAGTAGAAGAGTAAC	934
Oy	721	AACAAAGAGACACCATATCTGGACCAACACAGAAAGATGAAAGCGGCTCCATGCTGTG	780
Db	935	AACAAAGAGACACCATATCTGGACCAACACAGAAAGATGAAAGCGGCTCCATGCTGTG	994
Oy	781	CCGTGGGCCCAACACTTTCAAAGTTTGGCTGCCCGCGGGGGGAACCAATGCCAACATG	840
Db	995	CCGTGGGCCCAACACTTTCAAAGTTTGGCTGCCCGGGGGGAACCAATGCCAACATG	1054
Oy	841	CGGTGGCTGAAAAACGGGAAGATTTAAGCAGAGACATCGCATTTGGAGGCTCAAGAGTA	900
Db	1055	CGGTGGCTGAAAAACGGGAAGATTTAAGCAGAGACATCGCATTTGGAGGCTCAAGAGTA	1114
Oy	901	CGAAACACGACCTGAGACCTCATATTGGAAGTGTGTCCCATCTGCACAAAGGAAATTTAT	960
Db	1115	CGAAACACGACCTGAGACCTCATATTGGAAGTGTGTCCCATCTGCACAAAGGAAATTTAT	1174
Oy	961	ACCTGTGTGTGAGAAATGAATACGGGTCCCATCAATCACACGTACACACCTGATGTTTGTG	1020
Db	1175	ACCTGTGTGTGAGAAATGAATACGGGTCCCATCAATCACACGTACACACCTGATGTTTGTG	1234
Oy	1021	GAGCGATCGCCTCACCGCCCATCTCTCAAGCCGGAGTCCCGGCAAAATGCTCTCCACAGTG	1080
Db	1235	GAGCGATCGCCTCACCGCCCATCTCTCAAGCCGGAGTCCCGGCAAAATGCTCTCCACAGTG	1294
Oy	1081	GTCGGAGGACAGTAGAGTTTGTCTGCAAGGTTTACAGTATGCCAGGCCACATCCAG	1140
Db	1295	GTCGGAGGACAGTAGAGTTTGTCTGCAAGGTTTACAGTATGCCAGGCCACATCCAG	1354
Oy	1141	TGATTCAAAGCAGTGTGAAAAAAGCAGGAGTAAATACGGGCCCGACGGGGTGCCTTACCTC	1200
Db	1355	TGATTCAAAGCAGTGTGAAAAAAGCAGGAGTAAATACGGGCCCGACGGGGTGCCTTACCTC	1414
Oy	1201	AAGTGTTCAAAGCGCCGCGGTGTTAAACACACGACGAAAGAGATTGAGGTTCCTATATT	1260
Db	1415	AAGTGTTCAAAGCGCCGCGGTGTTAAACACACGACGAAAGAGATTGAGGTTCCTATATT	1426
Oy	1261	CGGAATGTAACTTTTGAAGAGCGCTGGGGAAATATACGTGTTGGCGGGTAATTCTATTGGG	1320
Db	1427	CGGAATGTAACTTTTGAAGAGCGCTGGGGAAATATACGTGTTGGCGGGTAATTCTATTGGG	1426
Oy	1321	ATATCTTTTACCTCTGCATGGTTGACAGATTCTGCCAGCGCCTGGAAAGAAAGAGATT	1380
Db	1427	ATATCTTTTACCTCTGCATGGTTGACAGATTCTGCCAGCGCCTGGAAAGAAAGAGATT	1426
Oy	1381	ACAGCTTCCCAAGACTACCTGGAGATATAGCAATTACTATAGGGGCTCTTAAATCGCC	1440
Db	1427	ACAGCTTCCCAAGACTACCTGGAGATATAGCAATTACTATAGGGGCTCTTAAATCGCC	1426

QY 1441 TGTATGCTGTAACAGTATCTCTGTGCCAATGAAGAACAAGCAAGAAAGCCAGACTTC 1500
Db 1427 ----- 1426
QY 1501 AGCAGCCAGCCGGCTGTGCACAAAGCTATCCCCCTGCGGAGACAGTAAACA 1560
Db 1427 ----- 1426
QY 1561 GTTTCGGCTGAGTCCAGCTCTCCATGACATCCAAACACCCCGGTGGAGATTAACACA 1620
Db 1427 GTTTCGGCTGAGTCCAGCTCTCCATGACATCCAAACACCCCGGTGGAGATTAACACA 1486
QY 1621 CGCCTCTCTTCAACGGCAGACACCCCATGCTGCGAGGGTCTCCAGTATGAATCTCA 1680
Db 1487 CGCCTCTCTTCAACGGCAGACACCCCATGCTGCGAGGGTCTCCAGTATGAATCTCA 1546
QY 1681 GAGGACCCAAATGGGGGCTTCCAAAGATTAACCTGACACTGGGCAAGCCCTGGAGAA 1740
Db 1547 GAGGACCCAAATGGGGGCTTCCAAAGATTAACCTGACACTGGGCAAGCCCTGGAGAA 1606
QY 1741 GGTTCCTTTGGCAAGTGTCTATGCGGGAAGCAGTGGGAATTCACAAAGACCAAGCC 1800
Db 1607 GGTTCCTTTGGCAAGTGTCTATGCGGGAAGCAGTGGGAATTCACAAAGACCAAGCC 1666
QY 1801 GAGGCGGTACCGTGGCCGTGAAGATGTGTAAGATGATGCCACAGAGAAAGCCTTCT 1860
Db 1667 GAGGCGGTACCGTGGCCGTGAAGATGTGTAAGATGATGCCACAGAGAAAGCCTTCT 1726
QY 1861 GATCTGCTGTCAGAGATGAGATGATGAAGATGATGGGAAACAAAGAAATATCATAAAT 1920
Db 1727 GATCTGCTGTCAGAGATGAGATGATGAAGATGATGGGAAACAAAGAAATATCATAAAT 1786
QY 1921 CTTCCTTGAGACTGCACACAGATGGGCTCTCTATGTCATAGTATGATGCTCTTAA 1980
Db 1787 CTTCCTTGAGACTGCACACAGATGGGCTCTCTATGTCATAGTATGATGCTCTTAA 1846
QY 1981 GGCACCTCCGAGAAATATCCGAGCCGAGGAGCCACCCGGGATGAGATGCTCTATGAC 2040
Db 1847 GGCACCTCCGAGAAATATCCGAGCCGAGGAGCCACCCGGGATGAGATGCTCTATGAC 1906
QY 2041 ATTACCGTCTCTGAGAGAGAGATGACCTTCAAGGATGGTGTGTCATGACCTACAG 2100
Db 1907 ATTACCGTCTCTGAGAGAGAGATGACCTTCAAGGATGGTGTGTCATGACCTACAG 1966
QY 2101 CTGGCCAGAGGATGAGATGCTTGGCTTCCAAAAATGTAATTCATGAGATTTAGAGCC 2160
Db 1967 CTGGCCAGAGGATGAGATGCTTGGCTTCCAAAAATGTAATTCATGAGATTTAGAGCC 2026
QY 2161 AGAAATGTTTGTGTAACAGAAACAATGATGAAATATGACAGCTTTGGAGCTCCGACA 2220
Db 2027 AGAAATGTTTGTGTAACAGAAACAATGATGAAATATGACAGCTTTGGAGCTCCGACA 2086
QY 2221 GATATCAACATATAGACTATTACAAAAAGACCACCAATGGCGGCTTCCAGTCAAGTGG 2280
Db 2087 GATATCAACATATAGACTATTACAAAAAGACCACCAATGGCGGCTTCCAGTCAAGTGG 2146
QY 2281 ATGGCTCCAGAGCCCTGTTTATAGAGATATCACTCATGAGATGATGCTGTCTTC 2340
Db 2147 ATGGCTCCAGAGCCCTGTTTATAGAGATATCACTCATGAGATGATGCTGTCTTC 2206
QY 2341 GGGGTGTAAATGTGGAGATCTTCACTTAAAGGGGCTGCGCTTACCCAGGGATTCGCGTG 2400
Db 2207 GGGGTGTAAATGTGGAGATCTTCACTTAAAGGGGCTGCGCTTACCCAGGGATTCGCGTG 2266
QY 2401 GAGGAACCTTTTAACCTGCTGAGAGAGACACAGATGATTAACCCAGCCAACTGCACC 2460
Db 2267 GAGGAACCTTTTAACCTGCTGAGAGAGACACAGATGATTAACCCAGCCAACTGCACC 2326
QY 2461 AACGAACCTGATCATGATGAGGAGCTGTGGCATGAGTGGCCCTCCCAAGACCAACG 2520
Db 2327 AACGAACCTGATCATGATGAGGAGCTGTGGCATGAGTGGCCCTCCCAAGACCAACG 2386
QY 2521 TTCAAGCAGTTGTAGAAAGACTGTGATGAAATTTCTCACTCTACACAAATGAGAGATAC 2580

Db 2387 TTTAAGCAGTTGGTAGAAGCTTGGATCGAAATTCCTACTCTCCAAACCAATGAGAAATAC 2446
QY 2581 TTGACCTCAGCCAACTCTCGAAGATATTCACCTAGTATACCTGACACAGAAATTTCT 2640
Db 2447 TTGACCTCAGCCAACTCTCGAAGATATTCACCTAGTATACCTGACACAGAAATTTCT 2506
QY 2641 TGTTCCTCAGAGATGATCTGTTTTTCTCCAGAGCCCATGCTTACCAACATGCTT 2700
Db 2507 TGTTCCTCAGAGATGATCTGTTTTTCTCCAGAGCCCATGCTTACCAACATGCTT 2566
QY 2701 CCTCAGATCCACATPAAPAAAGCAGTGTAAACATGATGATGCTGTCTGCTGCC 2760
Db 2567 CCTCAGATCCACATPAAPAAAGCAGTGTAAACATGATGATGCTGTCTGCTGCC 2626
QY 2761 CAACAGCAGCAGCTGGAACCTAGCTACCTGAGCAGGAGACCATGCTCCAGACC 2820
Db 2627 CAACAGCAGCAGCTGGAACCTAGCTACCTGAGCAGGAGACCATGCTCCAGACC 2686
QY 2821 TTGTTCTCCACTTGTATATATGATCAGAGAGTAAATTAATGGAAAAATATCAGCA 2880
Db 2687 TTGTTCTCCACTTGTATATATGATCAGAGAGTAAATTAATGGAAAAATATCAGCA 2746
QY 2881 TATGTAAAGATTTTATACAGTTGAAACTTGAATCTTCCCGAGAGAGAAAGATT 2940
Db 2747 TATGTAAAGATTTTATACAGTTGAAACTTGAATCTTCCCGAGAGAGAAAGATT 2806
QY 2941 TCTGAGCAGTGGACTGCCAAGCCACCATGTAACCCCTCCTACCTGCGCTTCTG 3000
Db 2807 TCTGAGCAGTGGACTGCCAAGCCACCATGTAACCCCTCCTACCTGCGCTTCTG 2866
QY 3001 GCTGAGCAGCTAGACATCAAGTGGAGTGGCTGCTTCTGCTTCTGTTAAATTTGTA 3060
Db 2867 GCTGAGCAGCTAGACATCAAGTGGAGTGGCTGCTTCTGCTTCTGTTAAATTTGTA 2926
QY 3061 TAAATGAGAAATTTATGTCAGACACACTTACAGACACAAATGCAATATATGAGTGC 3120
Db 2927 TAAATGAGAAATTTATGTCAGACACACTTACAGACACAAATGCAATATATGAGTGC 2986
QY 3121 TGGATGATGTAATATATATTCAAATTAATGATATATATATATATATATTAACAAGAGT 3180
Db 2987 TGGATGATGTAATATATATTCAAATTAATGATATATATATATATATATTAACAAGAGT 3046
QY 3181 TATTTTGTATGATTTTAAATGATGATGCCAATGCAACCTAAGAAATTTGCTCTT 3240
Db 3047 TATTTTGTATGATTTTAAATGATGATGCCAATGCAACCTAAGAAATTTGCTCTT 3106
QY 3241 TTTTAAATGCTATTTGCTAAATGCTGTCTTACACATTAATTTCTTAATTTCCACGAGCA 3300
Db 3107 TTTTAAATGCTATTTGCTAAATGCTGTCTTACACATTAATTTCTTAATTTCCACGAGCA 3166
QY 3301 GAGGTGAAAAATACTTTTGTTCAGGAAAAATGCTAATGCTTAATTTAATAAAT 3360
Db 3167 GAGGTGAAAAATACTTTTGTTCAGGAAAAATGCTAATGCTTAATTTAATAAAT 3226
QY 3361 TGGTAAATATACAAACAA 3378
Db 3227 TGGTAAATATACAAACAA 3244

RESULT 12
AF211257 3809 bp mRNA linear MAM 05-JAN-2000
LOCUS
DEFINITION
complete cds.
ACCESSION
AF211257
VERSION
AF211257.1 GI:6671356
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 3809)

[illegible]

KEYWORDS	fibroblast growth factor receptor 2; ligand binding.
SOURCE	Homo sapiens placenta cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Dell, K.R. and Williams, L.T.
TITLE	1 (bases 1 to 3080)
JOURNAL	A novel form of fibroblast growth factor receptor 2. Alternative
MEDLINE	splitting of the third immunoglobulin-like domain confers ligand
PUBMED	binding specificity
FEATURES	J. Biol. Chem. 267 (29), 21225-21229 (1992)
source	1400433
gene	location/Qualifiers
CDS	1..3080
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/map="10q26"
	/feature_type="placenta"
	1..3080
	/gene="FCGR2"
	612..3080
	/gene="FCGR2"
	/note="human FCGR2 IIb"
	/codon_start=1
	/product="fibroblast growth factor receptor 2"
	/protein_id="AA52449.1"
	/db_xref="GI:182567"
	/db_xref="GDB:600-127-273"
	/translation="MWSMGRITCLVVTMTATLSLRPSFLVETDTLEPEPPKTYD
	/SQQEYVAAPESLEVRCLLDAVIASTTKDGHVLPNNRVLLIGETVLQIGAPVROS
	GLYATASRTVDSEITWYFMVAVTDAISGDEDEDTDGAEDSEVSNKRAPWTNTE
	KMERILHVPAAVTYKFRCPAGCAPDMPTMRLKNGEKFOEHRIGYKVRQHSILMT
	ESVYSDKQNTGVYENEGYSINTYHLIDYVERPNRPILQAGLPANAATVYGVDFEE
	VCKVYSDQPHIOWIKHVEKNGSYRPGGLYLVKLVKSGTSSNAEVLAFNTEAD
	AGEYICKRYSNIGQANDSAKLTPLVKKOAPRREKEITASPRLEIATYIGVPLIACM
	VVYTLCKMKNTTKRDESSQPAVHKLRKRLPLRQRYVSAESSMSMNSPIRYRIT
	RLSTADTPMLAGVSEYELPEDPKMERPRDVLTKRPLGEGFEQVYMAEAVGIDKDK
	PKEAVTAYVNLKIDATPEKDLSDLVSEEMMKIKGNHINLLGACTQDGLVIVYE
	YASKNLTREYVLRARPCMEYSYDINRPEBOMTKGLVSTYOLARMEYLAQKIC
	HRDLARNVLTENNVMKIDAGFLARDINLDYKKTNGSLPYKMAPEALPDRVYVY
	HOSDWFSVGLWMEITFLGSGPYDGIPEELFKLKEGRMDKPAKCNELNYMMRDC
	WHAVPSORPTKQLYEIDLRIITLTITNEEYIDLQSPLEQYSPSYPDRSSCSDDDS
	FSPDPYEPCLPQYPIHNGSVK"
BASE COUNT	777 a 814 c 868 g 621 t
ORIGIN	
Query Match.	91.0%; Score 2603.6; DB 9; Length 3080;
Best Local Similarity	97.3%; Pred. No. 0;
Matches 2674; Conservative	0; Mismatches 59; Indels 15; Gaps 2.

Db	639	CTGGCTGGTGCACACTGATGCACTCTTGCCCGCCGCCCTCTCTCACTTAACTTAAAG	698
Qy	361	GATACACACATTATAGAGCCAGAGAGCCACCACCAATACCAATCTCTCAACCAAGATG	420
Db	699	GATACACACATTATAGAGCCAGAGAGCCACCACCAATACCAATCTCTCAACCAAGATG	758
Qy	421	TACGTGCTGCCAGGGAGTGCGTAGAGGTGGCTCTCTGTTGAAGATGGCGCGTG	480
Db	759	TACGTGCTGCCAGGGAGTGCGTAGAGGTGGCTCTCTGTTGAAGATGGCGCGTG	818
Qy	481	ATCAGTTGGACTMAAGATGTGGGTGCACATTGGGGCCCAACATTAGACAGTCTTATTTGG	540
Db	819	ATCAGTTGGACTMAAGATGTGGGTGCACATTGGGGCCCAACATTAGACAGTCTTATTTGG	878
Qy	541	CAGTACTTCGAGATTAAGGGCGCCAGCCCTACAGACTCGCGCTCATAGCTTGACTAGCC	600
Db	879	GAGTACTTCGAGATTAAGGGCGCCAGCCCTACAGACTCGCGCTCATAGCTTGACTAGCC	938
Qy	601	AGTAGACTGTAGACACTGTGAACTTGTAATCTCATAGTGAATGTCCAGATGCCATCTCA	660
Db	939	AGTAGACTGTAGACACTGTGAACTTGTAATCTCATAGTGAATGTCCAGATGCCATCTCA	998
Qy	661	TCGGAGATGATGAGATGACACCCGATGGTGGGAAAGATTTTGTACGTGAAACAGTAAC	720
Db	999	TCGGAGATGATGAGATGACACCCGATGGTGGGAAAGATTTTGTACGTGAAACAGTAAC	1058
Qy	721	ACCAAGACAGACACTACTGTGACCAACACAGAAAGATGAAACCGGCTCATGCTGTG	780
Db	1059	ACCAAGACAGACACTACTGTGACCAACACAGAAAGATGAAACCGGCTCATGCTGTG	1118
Qy	781	CCGTGGGCGCAACTGTCTAAGTTTCGTGCGCCAGCCGGGGGGAACCCATGCCAACATG	840
Db	1119	CCGTGGGCGCAACTGTCTAAGTTTCGTGCGCCAGCCGGGGGGAACCCATGCCAACATG	1178
Qy	841	CGGTGGCGTGAAGAAACGGGAAGAGATTAAACACAGACACTGCGATTGGAGGCTACAAAGTA	900
Db	1179	CGGTGGCGTGAAGAAACGGGAAGAGATTAAACACAGACACTGCGATTGGAGGCTACAAAGTA	1238
Qy	901	CGAAACGAGCACTGAGCTCTCATTTATGAAAGTGTGTCCTCATCTGACAAAGGAAATTTAT	960
Db	1239	CGAAACGAGCACTGAGCTCTCATTTATGAAAGTGTGTCCTCATCTGACAAAGGAAATTTAT	1298
Qy	961	ACCTGTGTGTGGGAAGATGAAATACGGGTCCTCATACACAGTACACACTGGATGTTGTG	1020
Db	1299	ACCTGTGTGTGGGAAGATGAAATACGGGTCCTCATACACAGTACACACTGGATGTTGTG	1358
Qy	1021	GAGCGATGCGCTCACCGGCCCATCTTCAAGCGGACTCCCGGCAAAATGCTCCACAAGTG	1080
Db	1359	GAGCGATGCGCTCACCGGCCCATCTTCAAGCGGACTCCCGGCAAAATGCTCCACAAGTG	1418
Qy	1081	GTTCGAGGAGACGTAAAGATTTGTCTGAAGGTTTACAGTAAATGATGGCCAGGCCACATTCAG	1140
Db	1419	GTTCGAGGAGACGTAAAGATTTGTCTGAAGGTTTACAGTAAATGATGGCCAGGCCACATTCAG	1478
Qy	1141	TGGATCAAGACAGTGGAAAGAAAGCGCAGTAAATACGGGGCCGACCGGCTGCCCCTACCTC	1200
Db	1479	TGGATCAAGACAGTGGAAAGAAAGCGCAGTAAATACGGGGCCGACCGGCTGCCCCTACCTC	1538
Qy	1201	AAGGTTCTCAAGCGCCGCGGTGTTTAAACACACGAGCAAGAGATTAGGTTCTCTATATT	1260
Db	1539	AAGGTTCTCTCAACCACTCGGGGATTAATAATGTTCCAAATCCAAATGCTGTGCTGTG----	1593
Qy	1261	CGGAATGTAACTTTTGAAGACGCGTGGGAATATACGTGCTTGGCGGGTAATTCTTAATGGG	1320
Db	1594	-TCAATGTACCGAGCGGATGCTGGGGAATATATATGTAAGGTCCTCCAAATTATATAGG	1652
Qy	1321	ATACTCTTCACTGCACTGCTGATGAGAGTTCTGCC-----AGCGCTGGAAGAGAA	1371
Db	1653	CAGGCCAACCACTGCTGCGCTCACTGCTCACTCTGCCAAACAGCAACCGCTCTGGAAGAGAA	1712
Qy	1372	AACGATATTACAGTCTCCCAAGACACTGAGATGAGATAGCCATTACGTACATAGGGGCTTTC	1431
Db	1713	AACGATATTACAGTCTCCCAAGACACTGAGATGAGATAGCCATTACGTACATAGGGGCTTTC	1772

Qy	1432	TTAATCCGCTGTATGTGTGTAAACAGTACTCTGTGCGCAAAAGAACAACGACCAAGAG	1491
Db	1773	TTAATTCGCTTATATGTGTGTAAACAGTACTCTGTGCGCAAAAGAACAACGACCAAGAG	1832
Qy	1492	CCAGACTTCACACAGCACCGACCGGCTGTGGACAAGCTGCACAAACGTATCCCTCGCGAGA	1551
Db	1893	CCACACTTCACACACCGACCGGCTGTGGACAAGCTGCACAAACGTATCCCTCGCGAGA	1892
Qy	1552	CAGTAAACAGTTTCGGCTGAAGTCCAGAGCTCTCATGAACTCCAAACACCCGCTGTGAG	1611
Db	1893	CAGTAAACAGTTTCGGCTGAAGTCCAGAGCTCTCATGAACTCCAAACACCCGCTGTGAG	1952
Qy	1612	ATAACAACACCCCTCTCTTCAAGGCGAGACACCCCATGCTGTGCGAGGGGTCTCCAGTAT	1671
Db	1953	ATAACAACACCCCTCTCTTCAAGGCGAGACACCCCATGCTGTGCGAGGGGTCTCCAGTAT	2012
Qy	1672	GAACCTCCAGAGACCCAAAAATGGAGTTTCAAGATAAAGTGAAGTGCACAGCAAGCC	1731
Db	2013	GAACCTCCAGAGACCCAAAAATGGAGTTTCAAGATAAAGTGAAGTGCACAGCAAGCC	2072
Qy	1732	CTGGGAGAAGGTTCTTGGGGCAAGTGTCATGGCGGAGACAGTGGGAATTGACAAAGAC	1791
Db	2073	CTGGGAGAAGGTTCTTGGGGCAAGTGTCATGGCGGAGACAGTGGGAATTGACAAAGAC	2132
Qy	1792	AAGCCCAAGAGAGCGGTACACGTTGGCCGTAAGATGTTGAAAGATGATGCGCACAGAGAA	1851
Db	2133	AAGCCCAAGAGAGCGGTACACGTTGGCCGTAAGATGTTGAAAGATGATGCGCACAGAGAA	2192
Qy	1852	GACCTTTCATATCTGGTGTGAGAGATGAGATGATGAAGATGATTGGGAAACACAAAGAT	1911
Db	2193	GACCTTTCATATCTGGTGTGAGAGATGAGATGATGAAGATGATTGGGAAACACAAAGAT	2252
Qy	1912	ATCATAAATCTTTCTGGAGCCTCACACAGAGATGGGCTCTCATGTGATAGATGAGTAT	1971
Db	2253	ATCATAAATCTTTCTGGAGCCTCACACAGAGATGGGCTCTCATGTGATAGATGAGTAT	2312
Qy	1972	GCTCTAAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGGCGCACCCGGATGAGATAC	2031
Db	2313	GCTCTAAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGGCGCACCCGGATGAGATAC	2372
Qy	2032	TGCTATGACATTTAAACGCTGTCCCTGGAGGAGACATGATACCTTCAAGACATGGTGTATGC	2091
Db	2373	TGCTATGACATTTAAACGCTGTCCCTGGAGGAGACATGATACCTTCAAGACATGGTGTATGC	2432
Qy	2092	ACCTACCACTGGCCGAGAGCATGAGTACTTGGCTTCCCAAAAATGTATTCTACGAGAT	2151
Db	2433	ACCTACCACTGGCCGAGAGCATGAGTACTTGGCTTCCCAAAAATGTATTCTACGAGAT	2492
Qy	2152	TTAGCAGCCAGAAATGTTTTGGTAACAGAAAAACATGTGATGAAATATGCAGACTTTTGA	2211
Db	2493	TTAGCAGCCAGAAATGTTTTGGTAACAGAAAAACATGTGATGAAATATGCAGACTTTTGA	2552
Qy	2212	CTGCGCAGAGATATCAACAATATAGACTTTTACAAAAAGACACCAATGGCGGCTTCCA	2271
Db	2553	CTGCGCAGAGATATCAACAATATAGACTTTTACAAAAAGACACCAATGGCGGCTTCCA	2612
Qy	2272	GTCAGTGGATGGCTCCACAAAGCCCTGTTGATAGATATACACTCATCAGAGTGAATGTC	2331
Db	2613	GTCAGTGGATGGCTCCACAAAGCCCTGTTGATAGATATACACTCATCAGAGTGAATGTC	2672
Qy	2332	TGCTCTTCGGGGTGTAAATGTGGGAGATCTTACACTTGTGGGGGCTCGCCCAACGAGG	2391
Db	2673	TGCTCTTCGGGGTGTAAATGTGGGAGATCTTACACTTGTGGGGGCTCGCCCAACGAGG	2732
Qy	2392	ATTCCCGTGGAGAACTTTTAAAGTCTGAAGAGACACAGATGGATTAAGCAGGC	2451
Db	2733	ATTCCCGTGGAGAACTTTTAAAGTCTGAAGAGACACAGATGGATTAAGCAGGC	2792
Qy	2452	AACTGCACCAAGCAACTCTACATGATGATGAGAGACTGTGGCAATGAGATGCGCTCCAG	2511
Db	2793	AACTGCACCAAGCAACTCTACATGATGATGAGAGACTGTGGCAATGAGATGCGCTCCAG	2852

	Query Match	Best local Similarity	Matches	Score	Pred.	No.	Mismatches	Indels	Gaps
OY	274	ATGGTCAGCTGGGCGTCTTCATCTGCCTGCGTGCGTACCACTGGAACCTGTCCCTG	333	57.8%	DB 6;	Length 2466;			
Dd	1	ATGGTCAGCTGGGCGTCTTCATCTGCCTGCGTGCGTACCACTGGAACCTGTCCCTG	60						
OY	334	GGCGGCGCCTCTTACTGATTACTTAGAGATACACATTAGAACCAGAAAGGCCAACCAACC	393						
Dd	61	GGCGGCGCCTCTTACTGATTACTTAGAGATACACATTAGAACCAGAAAGGCCAACCAACC	120						
OY	394	AAATACCAAATCTCCAAACAGAAATGTACAGTGGCGTGGCCAGAGGAGTTGCTGAGGTG	453						
Dd	121	AAATACCAAATCTCCAAACAGAAATGTACAGTGGCGTGGCCAGAGGAGTTGCTGAGGTG	180						
OY	454	CGCTCCGCTGTAAAAGATCCGCCGTGATCAAGTGGACTAAGATGGGGTCCACTTGGGG	513						
Dd	181	CGCTCCGCTGTAAAAGATCCGCCGTGATCAAGTGGACTAAGATGGGGTCCACTTGGGG	240						
OY	514	CCCACAATATAGACAGTCTTAATGGGGAGATCTGCAGATATAAGGGGGGCCACCCCTAGA	573						
Dd	241	CCCACAATATAGACAGTCTTAATGGGGAGATCTGCAGATATAAGGGGGGCCACCCCTAGA	300						
OY	574	GACTCGGCGCTTATGCTTGTACTGCCAGTAGAGACTAGACAGTGAACCTTGGTACTTC	633						
Dd	301	GACTCGGCGCTTATGCTTGTACTGCCAGTAGAGACTAGACAGTGAACCTTGGTACTTC	360						
OY	634	ATGGGATATGTCACAGATAGCATCTCATCCGGAATATAGAGATGACACACCGATGTGCG	693						
Dd	361	ATGGGATATGTCACAGATAGCATCTCATCCGGAATATAGAGATGACACACCGATGTGCG	420						
OY	694	GAAGATTTTGTCACTGAGAACAGTACAAACAAAGAGACACCATATCTGTGACCAACACAGAA	753						


```

Db 421 GAAGATTTTGTGAGTAAGTAACAGTAACAGAGAGACCATAGTGGACCAACAGAA 480
Oy 754 AAGATGAAAAAGGGCTCCATGCTGTGCTGGGCCCCAACAGTGTGAAGTTTGGCTGCCCA 813
Db 481 AAGATGAAAAAGGGCTCATGCTGTGCTGGGCCCCAACAGTGTGAAGTTTGGCTGCCCA 540
Oy 814 GCGGGGGGGAACCAATGCCAACATGCGGTGGCTGAAAAAGGGAAGGAGTTTAAAGCAG 873
Db 541 GCGGGGGGGAACCAATGCCAACATGCGGTGGCTGAAAAAGGGAAGGAGTTTAAAGCAG 600
Oy 874 GAGCATTCGATTTGGAGGCTTCAAGAGTACGAACACGACCTGAGAGCTCATTTATGAAAT 933
Db 601 GAGCATTCGATTTGGAGGCTTCAAGAGTACGAACACGACCTGAGAGCTCATTTATGAAAT 660
Oy 934 GTGTGTCATCTGACAAAGGAATTTATCTGTGTGTGGAGAAATATAACGGGTGCATC 993
Db 661 GTGTGTCATCTGACAAAGGAATTTATCTGTGTGTGGAGAAATATAACGGGTGCATC 720
Oy 994 AATCACACCTACCAACCTGATGTTGTGGAGCATCGCTTCACCGCCCATCTCCAAAGCC 1053
Db 721 AATCACACCTACCAACCTGATGTTGTGGAGCATCGCTTCACCGCCCATCTCCAAAGCC 780
Oy 1054 GGAATGCGGCAAAATGCTCTCACAGTGTGTGGAGAGACCTAGAGTTTGTCTGCAAGCTT 1113
Db 781 GGAATGCGGCAAAATGCTCTCACAGTGTGTGGAGAGACCTAGAGTTTGTCTGCAAGCTT 840
Oy 1114 TACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1173
Db 841 TACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Oy 1174 TACGGGCGGCAAGGGGCTGCTTACCTCAGAGTGTCTCAAGGCGCGGTGTTAAACACCA 1233
Db 901 TACGGGCGGCAAGGGGCTGCTTACCTCAGAGTGTCTCAAGGCGCGGTGTTAAACACCA 960
Oy 1234 GACAAAGATTTGAGTTTCTATATTCGGAATGATTAATCTTTTGGAGAGCGGTGGGAATAT 1293
Db 961 GACAAAGATTTGAGTTTCTATATTCGGAATGATTAATCTTTTGGAGAGCGGTGGGAATAT 1020
Oy 1294 ACGTCTTGGGGGATTAATCTTATTTGGGATATCTTTTACCTCTGCTGATGATGATGATGAT 1353
Db 1021 ACGTCTTGGGGGATTAATCTTATTTGGGATATCTTTTACCTCTGCTGATGATGATGATGAT 1080
Oy 1354 CCAGCGCTGGAAGAAAGAGATTAACAGCTTCCCGAGACCTGAGAGATGAGCATT 1413
Db 1081 CCAGCGCTGGAAGAAAGAGATTAACAGCTTCCCGAGACCTGAGAGATGAGCATT 1140
Oy 1414 TACTGATAGGGGCTCTTCTTAATCGCCTGTATGCTGATTAACAGTCACTCTGCGCAATG 1473
Db 1141 TACTGATAGGGGCTCTTCTTAATCGCCTGTATGCTGATTAACAGTCACTCTGCGCAATG 1200
Oy 1474 AAGAACACGACCAAGAACGACGACTTCAAGCAGCGCGGTGTGACAAAGCTAACCAAA 1533
Db 1201 AAGAACACGACCAAGAACGACGACTTCAAGCAGCGCGGTGTGACAAAGCTAACCAAA 1260
Oy 1534 CGTATCCCTCGCGGAGAGAGATTAACAGTTCGCGTGAAGTCACTCTGCAATGATCTC 1593
Db 1261 CGTATCCCTCGCGGAGAGAGATTAACAGTTCGCGTGAAGTCACTCTGCAATGATCTC 1320
Oy 1594 AACACCCGCTGTGTGAGAGATTAACAGCAGCCTCTCTTCAACGCGAGACACCCCATGCTG 1653
Db 1321 AACACCCGCTGTGTGAGAGATTAACAGCAGCCTCTCTTCAACGCGAGACACCCCATGCTG 1380
Oy 1654 GCAGGGGCTCTCGAGTATGAAGTTCAGAGAGACCAAAATGGAGTTTCAAGAGATTAAG 1713
Db 1381 GCAGGGGCTCTCGAGTATGAAGTTCAGAGAGACCAAAATGGAGTTTCAAGAGATTAAG 1440
Oy 1714 CTGACACTGTGGCAAGCCCTGTGGAGAGAGTGTCTTTGGGCAAGTGTCTATGGCGAAACA 1773
Db 1441 CTGACACTGTGGCAAGCCCTGTGGAGAGAGTGTCTTTGGGCAAGTGTCTATGGCGAAACA 1500
Oy 1774 GTGGGAATTTGACAAAGACAGCCCAAGAGAGCGGTCAACCGTGGCGCTGAAGATGTTGAAA 1833

```

```

Db 1501 GTGGGAATTTGACAAAGACAAACCCCAAGAGAGCGGTCAACCGTGGCCGTGAAGATGTTGAAA 1560
Oy 1834 GATGATGCGCACAGAGAAAGACCTTTCTGATCTGTGTGTCAGAGATGAGATGATGATGATG 1893
Db 1561 GATGATGCGCACAGAGAAAGACCTTTCTGATCTGTGTGTCAGAGATGAGATGATGATGATG 1620
Oy 1894 ATTGGGAAACACAGAAATATCATTAATCTTGTGAGGCTTCACACAGAGATGGGCTCTCTC 1953
Db 1621 ATTGGGAAACACAGAAATATCATTAATCTTGTGAGGCTTCACACAGAGATGGGCTCTCTC 1680
Oy 1954 TATGTCATAGTTGAGTATGACCTCTTAAAGCAACCTCCAGAAATACCTCCAGCCGAGG 2013
Db 1681 TATGTCATAGTTGAGTATGACCTCTTAAAGCAACCTCCAGAAATACCTCCAGCCGAGG 1740
Oy 2014 CCACCCGGAGTGGAGTACTCCTATGACATTTAAACCTGTCTTCTGAGAGACATGACCTTC 2073
Db 1741 CCACCCGGAGTGGAGTACTCCTATGACATTTAAACCTGTCTTCTGAGAGACATGACCTTC 1800
Oy 2074 AAGGACTGTGTGATGACACCTTACAGCTGAGGCGACAGGCAATGATGATGATGATGATGAT 2133
Db 1801 AAGGACTGTGTGATGACACCTTACAGCTGAGGCGACAGGCAATGATGATGATGATGATGAT 1860
Oy 2134 AATGATTTATCATGAGATTTAGACAGCCAGAAATGTTTGTAAACGAAACAAATGTATG 2193
Db 1861 AATGATTTATCATGAGATTTAGACAGCCAGAAATGTTTGTAAACGAAACAAATGTATG 1920
Oy 2194 AAAATATGACAGATTTTGTGACTGCGCCAGAGATATCAACATATATGATATATGATATG 2253
Db 1921 AAAATATGACAGATTTTGTGACTGCGCCAGAGATATCAACATATATGATATATGATATG 1980
Oy 2254 ACCAATGGGCGGCTTCCAGATCAAGTATGCTCCAGAGAGCCCTGTTGATGATGATGATGAT 2313
Db 1981 ACCAATGGGCGGCTTCCAGATCAAGTATGCTCCAGAGAGCCCTGTTGATGATGATGATGAT 2040
Oy 2314 ACTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2373
Db 2041 ACTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Oy 2374 GCGTGGCCCTTACCCAGAGATGCTGCGTGGAGAACTTTTAACTGCTGAAGAGAGAGAC 2433
Db 2101 GCGTGGCCCTTACCCAGAGATGCTGCGTGGAGAACTTTTAACTGCTGAAGAGAGAGAC 2160
Oy 2434 AGAATGATTAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2493
Db 2161 AGAATGATTAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2220
Oy 2494 CATGCAAGTGGCTTCCAGAGACCAAGCTTCAAGCAATGTTGTAAGAGACTTGCATGAAT 2553
Db 2221 CATGCAAGTGGCTTCCAGAGACCAAGCTTCAAGCAATGTTGTAAGAGACTTGCATGAAT 2280
Oy 2554 CTCACCTCTCAACAGCAATGAGAACTTGTGAGACCTGAGCCAACTCTCGAACAGATTA 2613
Db 2281 CTCACCTCTCAACAGCAATGAGAACTTGTGAGACCTGAGCCAACTCTCGAACAGATTA 2340
Oy 2614 CTTAGTTACCTTACACAGAAATGTTCTTGTCTTCAAGAGATGATGATGATGATGATGAT 2673
Db 2341 CTTAGTTACCTTACACAGAAATGTTCTTGTCTTCAAGAGATGATGATGATGATGATGAT 2400
Oy 2674 GACCCCATGCTTACAGAAACATGCTTCTCACTATGACACATTAAGGCAAGTGTAA 2733
Db 2401 GACCCCATGCTTACAGAAACATGCTTCTCACTATGACACATTAAGGCAAGTGTAA 2460
Oy 2734 ACATGA 2739
Db 2461 ACATGA 2466

```

```

RESULT 15
LOCUS HUMTK14 2481 bp mRNA linear PRI 14-JAN-1995
DEFINITION Human fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M55614 M37715
VERSION M55614.1 GI:339710

```


KEYWORDS TK14 protein: fibroblast growth factor receptor; protein-tyrosine kinase.
SOURCE Human, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. Houssaint, E., Blanquet, P.R., Champion-Arnaud, P., Gesnel, M.C., Torriglia, A., Courtois, Y., and Breathnach, R.
AUTHORS Related fibroblast growth factor receptor genes exist in the human genome
TITLE
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (20), 8180-8184 (1990)
MEDLINE 91045961
PUBMED 2172978
FEATURES
source Location/Qualifiers
1..2481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="tumor"
1..2481
/gene="Ig f receptor"
13..2481
/gene="Ig f receptor"
/codon_start=1
/product="TK14 protein"
/protein_id="AA61188.1"
/db_xref="GI:339711"
/translation="MWSMGREFICLVVVTMATLSARPSFSLVEDTLEPERPPKYYOI
SOPHYVAAPGESLEVRCLMDAIVISMTKGVHLGPNRRYLIGETIQIGATPRDS
GLKERTATDSEWYPMVAVTDAISSGDEDDTDGAEDEYSESNKRAVPTNTE
KMERLHAVPANTYKFKPCPAGGNMPTMKMKNGKROKHIGCYVVRQHSLLM
ESVPSDKGNTGVENEYGSINHTYHLADVVERHPD1LOAGLPAANSTVVGGLVE
VCKVSDAOPHIOWIKHVEKNGSKYGPGLPYLKYKLTAKAGVNTTKELEVYIRN
VTFEDAGYTCIAGNSIGISFHSAMLTVLPAPGREKETASPDYETLITCIGYFLIA
CMVVYIILCRMKNTFKRDPSSOPAVHKLTRIPLRQVSAESSSNSTPLVRITTT
RLSSADTQPMLAGVSEYELPDPKPEPRDRLTLGKPEGECRGQVYAAEAVGIDKDK
PKEAVTVAKMLKXDATPEKDLSDLYSEEMKMKIGKHNITLNLACTQDPLVYIE
YASKNLALEYLRARPPGMEYSTDINRVPEQMTFKDLSTYDOLARMEYLAQKCI
HRDLARNAVLTENNVMKIDFGIARDINIDYKKTNGRLPYKMAPEALPFRVYT
HOSDWMSFVLMELFTLGGSPYDGIPIVEELFKLKEGRMDKPMANCTNELYMMMRDC
WHAVSORPTEKQVEDLDRLTLTLTNEEYLDLSQPLEOYSPSYPDTRSSGSDDSV
FSPDPMPEPLPQYPHINSVKT"

BASE COUNT 673 a 609 c 660 g 539 t
ORIGIN

Query Match 57.1% Score 2437; DB 9; Length 2481;
Best Local Similarity 99.4% Pred. No. 0;
Matches 2472; Conservative 0; Mismatches 0; Indels 15; Gaps 2;

QY 262 GTACCGTAACCATGTCAGTGGGGTGTTCATCGCTGCTGCTGTCACCATGCA 321
DB 1 GGTACCGTAACCATGTCAGTGGGGTGTTCATCGCTGCTGCTGTCACCATGCA 60
QY 322 ACCTTGCTCCGCGCCGCCCTCTTCAAGTTAGTGAAGATACACATTAGAGCCAGA 381
DB 61 ACCTTGCTCCGCGCGCCGCCCTCTTCAAGTTAGTGAAGATACACATTAGAGCCAGA 120
QY 382 GAGCCACCAACCAATTAACCAATCTCTCAACCAAGTGTACGTGGCGCCAGGGAG 441
DB 121 GAGCCACCAACCAATTAACCAATCTCTCAACCAAGTGTACGTGGCGCCAGGGAG 180
QY 442 TCGGTAGAGTCCGCTGCTGTTGAAGATGCCCGGTGATCAGTTGACATGAAGATGG 501
DB 181 TCGGTAGAGTCCGCTGCTGTTGAAGATGCCCGGTGATCAGTTGACATGAAGATGG 240
QY 502 GTGCACTTGGGGCCCAACATAGACAGTGTATTGGGGAGTACTTCAGATAAAGGC 561
DB 241 GTGCACTTGGGGCCCAACATAGACAGTGTATTGGGGAGTACTTCAGATAAAGGC 300
QY 562 GCCAGGCTTAGAGACTCGGCGCTATGCTGTACTGCAATAGACATGTGAGACGTGA 621
DB 301 GCCAGGCTTAGAGACTCGGCGCTATGCTGTACTGCAATAGACATGTGAGACGTGA 360

QY 622 ACTTGCTACTCATGCTGATGTCACAGATGCCATCTCATCCGGAGATGATGAGATGAC 681
DB 361 ACTTGCTACTCATGCTGATGTCACAGATGCCATCTCATCCGGAGATGATGAGATGAC 420
QY 682 ACCGATGTCGCGAAGATTGTTGTACGTAGAACAGTAAACAAAGAGACACCATATCTGG 741
DB 421 ACCGATGTCGCGAAGATTGTTGTACGTAGAACAGTAAACAAAGAGACACCATATCTGG 480
QY 742 ACCAACACGAAAAGATGGAAGAGCGGCTCATGCTGTGCTGCGGCCAACATCTGCAAG 801
DB 481 ACCAACACGAAAAGATGGAAGAGCGGCTCATGCTGTGCTGCGGCCAACATCTGCAAG 540
QY 802 TTTGCGTCCCAAGCGCGGGGGAACCAATGCCACATGCGGTGCTGAAAACCGGAAG 861
DB 541 TTTGCGTCCCAAGCGCGGGGGAACCAATGCCACATGCGGTGCTGAAAACCGGAAG 600
QY 862 GAGTTTAAACAGAGACATGCAATTGGAGCTCAAGGTACGAAACAGACACTGAGCCCTC 921
DB 601 GAGTTTAAACAGAGACATGCAATTGGAGCTCAAGGTACGAAACAGACACTGAGCCCTC 660
QY 922 ATTATGGAAGTGTGCTCCATCTGCAAGGAATATATACCTGTGTGGTGAAGTAA 981
DB 661 ATTATGGAAGTGTGCTCCATCTGCAAGGAATATATACCTGTGTGGTGAAGTAA 720
QY 982 TAGGGGTCCATCATCACACGTACACCGTGGATGTTGTGGAGCGGATCCGCTCACCAGCC 1041
DB 721 TAGGGGTCCATCATCACACGTACACCGTGGATGTTGTGGAGCGGATCCGCTCACCAGCC 780
QY 1042 ATCTCCAAAGCGGAGCTGCGGCAAAATGCTTCACAGTGTGTCGAGAGAGATAGATT 1101
DB 781 ATCTCCAAAGCGGAGCTGCGGCAAAATGCTTCACAGTGTGTCGAGAGAGATAGATT 840
QY 1102 GCTGTCGAAGTTTACAGTATGTCGCCAGCCCAATCAGTGTGATCAAGCAGTGAAGAA 1161
DB 841 GCTGTCGAAGTTTACAGTATGTCGCCAGCCCAATCAGTGTGATCAAGCAGTGAAGAA 900
QY 1162 AAGGCACTAATATAGGCGCGGAGCGGCTGCGCTTC-----CTCAAGTTCTCAG 1212
DB 901 AAGGCACTAATATAGGCGCGGAGCGGCTGCGCTTC-----CTCAAGTTCTCAG 960
QY 1213 GCCGCGGCTGTTAACACACGAGACAAAGATGAGTTCTCTATATTCGGAATGTA 1272
DB 961 GCCGCGGCTGTTAACACACGAGACAAAGATGAGTTCTCTATATTCGGAATGTA 1020
QY 1273 TTTGAGACGCGTGGGGAATATACGTGCTTGGCGGTATCTTATGATATCTTTAC 1332
DB 1021 TTTGAGACGCGTGGGGAATATACGTGCTTGGCGGTATCTTATGATATCTTTAC 1080
QY 1333 TCTGCATGTTGACAGTTCTGCGACGCGCTGGAAGAGAAAAGATTAACAGTTCCCA 1392
DB 1081 TCTGCATGTTGACAGTTCTGCGACGCGCTGGAAGAGAAAAGATTAACAGTTCCCA 1140
QY 1393 GACTACCTGAGATATGACATTTACTGCTAGGGGTCTTCTTAATCGCCTGATGGTGA 1452
DB 1141 GACTACCTGAGATATGACATTTACTGCTAGGGGTCTTCTTAATCGCCTGATGGTGA 1200
QY 1453 ACAGTCATCTGTCGCGAATGAAGAACGACGCAAGAACGACGCTTACAGAGCACCG 1512
DB 1201 ACAGTCATCTGTCGCGAATGAAGAACGACGCAAGAACGACGCTTACAGAGCACCG 1260
QY 1513 GCTGTGCAAGAGTGCACCAAGTATCCCTGCGGAGACAGTAAAGTTTGGCTGAG 1572
DB 1261 GCTGTGCAAGAGTGCACCAAGTATCCCTGCGGAGAGAG-----GTTTGGGCTGAG 1314
QY 1573 TCCAGCTCTCATGATGATCCAAACACCCGCTGTGTGAGATTAACACACGCTCTCTCA 1632
DB 1315 TCCAGCTCTCATGATGATCCAAACACCCGCTGTGTGAGATTAACACACGCTCTCTCA 1374
QY 1633 ACAGCAGACACCCCATGCTGCGAGGGGTCTCCAGATATCACTTCAGAGAGACCCAAA 1692
DB 1375 ACAGCAGACACCCCATGCTGCGAGGGGTCTCCAGATATCACTTCAGAGAGACCCAAA 1434
QY 1693 TGGAGTTTCCAAAGATTAAGCTGACACTGCGGCAAGCCCTCGGACAAAGGTTCTTTGG 1752

Job time : 7248 secs

```
|||||
Db 1435 TGGGAGTTTCCAGAGATTAAGCTGACACTGGGCAAGCCCTGGGAAAGGTTGCTTTGGG 1494
OY 1753 CAAGTGTCTATGCGCGAAGCACTGGGAATTGCAAAAGACAAAGCCCAAGAGCGGCTCACG 1812
Db 1495 CAAGTGTCTATGCGCGAAGCACTGGGAATTGCAAAAGACAAAGCCCAAGAGCGGCTCACG 1554
OY 1813 GTGGCCGCTGAGAGATGTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGGTGTCA 1872
Db 1555 GTGGCCGCTGAGAGATGTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGGTGTCA 1614
OY 1873 GAGATGGAGATGATGAGATGATGGGAAACACAGAAATATCATTAATCTTCTTGAGCC 1932
Db 1615 GAGATGGAGATGATGAGATGATGGGAAACACAGAAATATCATTAATCTTCTTGAGCC 1674
OY 1933 TGCACACAGATGGGCGCTCTATGTATGATAGTTGAGTATGCCCTTAAAGCAACCTCCGA 1992
Db 1675 TGCACACAGATGGGCGCTCTATGTATGATAGTTGAGTATGCCCTTAAAGCAACCTCCGA 1734
OY 1993 GAATACCTCCGAGCCCGGAGCCGCGGATGAGTACTCCTATGACATTAAACGCTGT 2052
Db 1735 GAATACCTCCGAGCCCGGAGCCGCGGATGAGTACTCCTATGACATTAAACGCTGT 1794
OY 2053 CCTGAGAGCAGATGACCTTCAAGACCTGTGTGATGACACCTACACGCTGGCAGAGGC 2112
Db 1795 CCTGAGAGCAGATGACCTTCAAGACCTGTGTGATGACACCTACACGCTGGCAGAGGC 1854
OY 2113 ATGAGTACTTGGCTTCCCAAAATGTATTCATCGAGATTAGCAGCCAGAAATGTTTG 2172
Db 1855 ATGAGTACTTGGCTTCCCAAAATGTATTCATCGAGATTAGCAGCCAGAAATGTTTG 1914
OY 2173 GTACAGAAACAAATGTGAAATAGCAACTTGGACTGGCCAGATATCAACAT 2232
Db 1915 GTACAGAAACAAATGTGAAATAGCAACTTGGACTGGCCAGATATCAACAT 1974
OY 2233 ATGACTATTACAAAAGACACCAATGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAA 2292
Db 1975 ATGACTATTACAAAAGACACCAATGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAA 2034
OY 2293 GCCCTGTTTGATAGATATACACTCATGAGTGTGTGCTGCTTCCGGGCTTTAATG 2352
Db 2035 GCCCTGTTTGATAGATATACACTCATGAGTGTGTGCTGCTTCCGGGCTTTAATG 2094
OY 2353 TGGGACATCTGCTTAGGGGGCTGCGCCCTACCGAGGGATTCGGTGGAGAACTTTT 2412
Db 2095 TGGGACATCTGCTTAGGGGGCTGCGCCCTACCGAGGGATTCGGTGGAGAACTTTT 2154
OY 2413 AAGCTCTGAAGAGAGACACAGAAATGATTAAGCCAGCAAGTCAACCAAGAACTGTAC 2472
Db 2155 AAGCTCTGAAGAGAGACACAGAAATGATTAAGCCAGCAAGTCAACCAAGAACTGTAC 2214
OY 2473 ATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGTTCAAGCAGTTG 2532
Db 2215 ATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGTTCAAGCAGTTG 2274
OY 2533 GTAGAAGACTTGGATGAATTCACGTCACAAACCAATGAGAAATACATTGAGACTCAGC 2592
Db 2275 GTAGAAGACTTGGATGAATTCACGTCACAAACCAATGAGAAATACATTGAGACTCAGC 2334
OY 2593 CAACCTCTCGAAGACATTAATACCTAGTTACCTGACACAGAAAGTTCTTGTCTTCAGGA 2652
Db 2335 CAACCTCTCGAAGACATTAATACCTAGTTACCTGACACAGAAAGTTCTTGTCTTCAGGA 2394
OY 2653 GATGATTTCTTTTTTCTCCAGAGCCGATGGCTTAGAAGCATGCTCTCTCAGTATCCA 2712
Db 2395 GATGATTTCTTTTTTCTCCAGAGCCGATGGCTTAGAAGCATGCTCTCTCAGTATCCA 2454
OY 2713 CACATTAACGCGAGTGTAAACATGA 2739
Db 2455 CACATTAACGCGAGTGTAAACATGA 2481
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:52:46 ; Search time 550 Seconds

(without alignments)
17475.507 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 cccaaggaccactcttcg.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY-MNC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4268	100.0	4268	24	ABL64983
2	4268	100.0	4268	24	ABL66289
3	4268	100.0	4268	24	ABL68594
4	3381	79.2	3416	13	AAO21004
5	2670.4	62.6	3244	24	ABL61834
6	2466	57.8	2466	24	ABL91742
7	2188	51.3	2676	12	AAO14850
8	1817.2	42.6	1954	12	AAO14849
9	1689.6	39.6	2310	12	AAO14851

10	1642.8	38.5	2345	12	AAO14049
11	1642.8	38.5	2245	12	AAO10868
12	1367.6	32.0	2675	19	AAV19076
13	1367.6	32.0	2675	20	AAV19076
14	1318.8	30.9	1603	13	AAV19078
15	1276.4	29.9	2681	19	AAV19078
16	1276.4	29.9	2681	20	AAV19078
17	1188.2	27.8	3343	20	AAV19078
18	1188.2	27.7	2469	12	AAO13311
19	1182.2	27.7	2469	12	AAO13311
20	1182.2	27.7	3525	13	AAO27658
21	1177.2	27.6	3726	21	AAO18252
22	1164	27.3	2652	13	AAO21003
23	1159.2	27.2	2733	17	AAO31051
24	1147.2	26.9	2506	24	AAO1689
25	1141	26.7	3536	19	AAV44041
26	1131	26.5	3328	13	AAO20914
27	1127.8	26.4	2856	12	AAO10448
28	981.8	23.0	2421	24	ABL91743
29	981.8	23.0	5993	23	AAO34801
30	980.2	22.0	3829	24	ABO88193
31	980.2	22.0	3829	24	ABO88193
32	961.8	22.5	2049	23	AAO21622
33	956.2	22.4	8083	23	AAO34802
34	931.6	21.8	1079	12	AAO14846
35	897.2	21.0	2427	22	AAO54423
36	895.6	21.0	2427	22	AAO54406
37	895.6	21.0	2427	22	AAO54412
38	895.6	21.0	2427	22	AAO54414
39	895.6	21.0	2427	22	AAO54415
40	895.6	21.0	2427	22	AAO54416
41	895.6	21.0	2427	22	AAO54417
42	895.6	21.0	2427	22	AAO54418
43	895.6	21.0	2427	22	AAO54419
44	895.6	21.0	2427	22	AAO54420
45	895.6	21.0	2427	22	AAO54421

ALIGNMENTS

RESULT 1	ABL64983	standard; DNA; 4268 Bp.
XX	XX	ABL64983;
XX	XX	15-MAY-2002 (first entry)
XX	XX	Lung cancer related gene sequence SEQ ID NO:3320.
XX	XX	Human: cancer; colon; breast; ovary; kidney; thyroid;
XX	XX	stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
XX	XX	cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
XX	XX	gene; ds.
XX	XX	Homo sapiens.
XX	XX	MO200194629-A2.
XX	XX	13-DEC-2001.
XX	XX	30-MAY-2001; 2001MO-US10838.
XX	XX	05-JUN-2000; 2000US-209473P.
XX	XX	05-JUN-2000; 2000US-209531P.
XX	XX	18-SEP-2000; 2000US-231133P.
XX	XX	18-SEP-2000; 2000US-231617P.
XX	XX	20-SEP-2000; 2000US-234009P.
XX	XX	20-SEP-2000; 2000US-234034P.
XX	XX	20-SEP-2000; 2000US-234052P.
XX	XX	22-SEP-2000; 2000US-234505P.
XX	XX	22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 Sopet DR, Weaver Z;

WPI: 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set -
 Claim 1: SEQ ID 3320; 44pp: English.

The present invention describes a method (M1) for screening for an
 anti-neoplastic agent. The method involves exposing cells to a chemical
 agent to be tested for anti-neoplastic activity, determining a change in
 expression of at least one gene (I) of a signature gene set, where (I)
 comprises a sequence (S) selected from 8447 sequences (given in AB161664
 to AB170110), or is at least 95% identical to (S), where a change in
 expression is indicative of anti-neoplastic activity. (I) has cytostatic
 activity and can be used in gene therapy. M1 can be used for screening
 an anti-neoplastic agent, and can be used for producing a product which
 is the data collected with respect to the anti-neoplastic agent as a
 result of M1, and the data is sufficient to convey the chemical
 structure and/or properties of the agent. M1 can be used in the
 treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 4268 BP; 1199 A; 964 C; 1028 G; 1077 T; 0 other;

Query Match 100.0%; Score 4268; DB 24; Length 4268;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CCCAAGGACCACCTCTTCTGCGTTGGAGTTGTCCTCCACAAACCCGGGCTGCTGCTTTC 60
 |||||||

DB 1 CCCAAGGACCACCTCTTCTGCGTTGGAGTTGTCCTCCACAAACCCGGGCTGCTGCTTTC 60
 QY 61 TCCATCCCCGACCCGCGGGGCGGGGACACAGTGGGGAGGCGTTGCCATTG 120
 DB 61 TCCATCCCCGACCCGCGGGGCGGGGACACAGTGGGGAGGCGTTGCCATTG 120
 QY 121 AAGTACTGACGACGACGCGGACGCGCTGGTTCCTGAGACCCGACGCGCTGAAGCA 180
 DB 121 AAGTACTGACGACGACGCGGACGCGGCTGGTTCCTGAGACCCGACGCGCTGAAGCA 180
 QY 181 TTGGCGCTAGTCCATGCCCTGAGAGAACTGTGAGATGGGATTAACGTCCACATGGAGA 240
 DB 181 TTGGCGCTAGTCCATGCCCTGAGAGAACTGTGAGATGGGATTAACGTCCACATGGAGA 240
 QY 241 TATGGAAGAGACCGGGGATGGTACCGTAACATGGTACGTGGGTGCTTCATCTGC 300
 DB 241 TATGGAAGAGACCGGGGATGGTACCGTAACATGGTACGTGGGTGCTTCATCTGC 300
 QY 301 CTGTCGTGTGTCACCATGGCAACCTTGTCCCTGGCCGCGCCCTCTTCAGTTAGTTGAG 360
 DB 301 CTGTCGTGTGTCACCATGGCAACCTTGTCCCTGGCCGCGCCCTCTTCAGTTAGTTGAG 360
 QY 361 GATACCATTTAGAGCCAGAAAGCCACACCAATATCAATCTCTCAACCAAGAGTG 420
 DB 361 GATACCATTTAGAGCCAGAAAGCCACACCAATATCAATCTCTCAACCAAGAGTG 420
 QY 421 TACGTGGCTGGCGGAGGAGTGGCTAGAGTGGCGCTGCTGTAAGAAAGATGCCCGGTG 480
 DB 421 TACGTGGCTGGCGGAGGAGTGGCTAGAGTGGCGCTGCTGTAAGAAAGATGCCCGGTG 480
 QY 481 ATCAGTTGGACTAAGATGGGCTGCTGCTGGGCGCCCAACCAATAGACAGTCTTATTGGG 540
 DB 481 ATCAGTTGGACTAAGATGGGCTGCTGCTGGGCGCCCAACCAATAGACAGTCTTATTGGG 540
 QY 541 GAGTACTTGCAGATTAAGAGGGGCGCCAGCTAGACATCCCGGCTCTTACTTACTGCC 600
 DB 541 GAGTACTTGCAGATTAAGAGGGGCGCCAGCTAGACATCCCGGCTCTTACTTACTGCC 600
 QY 601 AGTAGACTGTAGACAGTGAACCTGTGACTTCAATGTGATGTGCACAGATGCCATCTCA 660
 DB 601 AGTAGACTGTAGACAGTGAACCTGTGACTTCAATGTGATGTGCACAGATGCCATCTCA 660
 QY 661 TCCGGAGATGATGAGATGACACCGGATGCGGAAATTTTGTCACTGACACAGTAAAC 720
 DB 661 TCCGGAGATGATGAGATGACACCGGATGCGGAAATTTTGTCACTGACACAGTAAAC 720
 QY 721 AACAGAAGACCACTACTGTGACCAACACAAAGATGAAAGCGGCTCCATGCTGTG 780
 DB 721 AACAGAAGACCACTACTGTGACCAACACAAAGATGAAAGCGGCTCCATGCTGTG 780
 QY 781 CCGTGGCCACACACTGTCAAGTTTGTGCTGCCAGCGGGGGGAACCCAAATGCCAACATG 840
 DB 781 CCGTGGCCACACACTGTCAAGTTTGTGCTGCCAGCGGGGGGAACCCAAATGCCAACATG 840
 QY 841 CGGTGGCTGAAAAACGGGAGAGTTTAAAGCAGACATCCGATTTGGAGGCTTCAAGGTA 900
 DB 841 CGGTGGCTGAAAAACGGGAGAGTTTAAAGCAGACATCCGATTTGGAGGCTTCAAGGTA 900
 QY 901 CGAAACCCGACCTGTGAGGCTCATTTATGAAAGTGTGTCCTGACAAAGGAAATTTAT 960
 DB 901 CGAAACCCGACCTGTGAGGCTCATTTATGAAAGTGTGTCCTGACAAAGGAAATTTAT 960
 QY 961 ACCTGTGTGTGAGAAATGATAGGGGTCCATCAATCAACGCTACACCTGTGATTTGTG 1020
 DB 961 ACCTGTGTGTGAGAAATGATAGGGGTCCATCAATCAACGCTACACCTGTGATTTGTG 1020
 QY 1021 GAGCGATCCCTTCACCGGCGCTTCTCCAAAGCCGAGCTCCGCGCAATGCTCCACAGTG 1080
 DB 1021 GAGCGATCCCTTCACCGGCGCTTCTCCAAAGCCGAGCTCCGCGCAATGCTCCACAGTG 1080
 QY 1081 GTGCGAGGAGAGTGTGAGTTTGTGCAAGGTTTACAGTATGATGCCAGCCACATCCAG 1140
 DB 1081 GTGCGAGGAGAGTGTGAGTTTGTGCAAGGTTTACAGTATGATGCCAGCCACATCCAG 1140

OY 1141 TGGATCAAGCAGCTGGAAAAGAACGGCAGTAATACGGGGCCGACGGGCTGCCCTACCTC 1200
DB 1141 TGGATCAAGCAGCTGGAAAAGAACGGCAGTAATACGGGGCCGACGGGCTGCCCTACCTC 1200
OY 1201 AAGGCTCTCAAGCCCGCGCTGTTAAACACCACGACGACAAAGAGATGAGGTTCTCTATAT 1260
DB 1201 AAGGCTCTCAAGCCCGCGCTGTTAAACACCACGACGACAAAGAGATGAGGTTCTCTATAT 1260
OY 1261 CGGAATGTAACCTTTTGAGAGCGCTGGGGAATATAGTGGCTGGCGGGTAATTTATTTGGG 1320
DB 1261 CGGAATGTAACCTTTTGAGAGCGCTGGGGAATATAGTGGCTGGCGGGTAATTTATTTGGG 1320
OY 1321 ATATCTTTCACTCTGATGTTGACAGTTTCCAGCGCTCGAAGAAAAGAGATTT 1380
DB 1321 ATATCTTTCACTCTGATGTTGACAGTTTCCAGCGCTCGAAGAAAAGAGATTT 1380
OY 1381 ACAGCTTCCCGACACTGATCGTGGAGATAGCCATTACTGATAGGGGCTCTTTAATGCC 1440
DB 1381 ACAGCTTCCCGACACTGATCGTGGAGATAGCCATTACTGATAGGGGCTCTTTAATGCC 1440
OY 1441 TGTATGTTGTAACAGTATCTCTGTGCGAATGAAAGACGACGACCAAGAGCCAGACTTC 1500
DB 1441 TGTATGTTGTAACAGTATCTCTGTGCGAATGAAAGACGACGACCAAGAGCCAGACTTC 1500
OY 1501 AGCAGCCAGCCGCGCTGTGCACAAAGCTGACCAAACTATCCCTTGGCGAGAGATTAACA 1560
DB 1501 AGCAGCCAGCCGCGCTGTGCACAAAGCTGACCAAACTATCCCTTGGCGAGACGATTAACA 1560
OY 1561 GTTTGGGCTGAGTCCAGCTCTCCATGAACTCCAGACCCCGCTGGTGAGATTAACACA 1620
DB 1561 GTTTGGGCTGAGTCCAGCTCTCCATGAACTCCAGACCCCGCTGGTGAGATTAACACA 1620
OY 1621 CGCCTCTCTTCAACGCGACAGACACCCCATGTGCGAGGGGTCTCGAGATATCACTCCA 1680
DB 1621 CGCCTCTCTTCAACGCGACAGACACCCCATGTGCGAGGGGTCTCGAGATATCACTCCA 1680
OY 1681 GAGGAGCCCAAAATGGGAGATTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
DB 1681 GAGGAGCCCAAAATGGGAGATTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
OY 1741 GGTTCCTTTGGGCAAGTGTGATGCGGAAAGAGAGTGGGAATGACAAAGACAAAGCCCAAG 1800
DB 1741 GGTTCCTTTGGGCAAGTGTGATGCGGAAAGAGAGTGGGAATGACAAAGACAAAGCCCAAG 1800
OY 1801 GAGGCGGTACCGGTGCGCGTGAAGATGTTGAAAAGATGATGCCACAGAGAAACCTTTCT 1860
DB 1801 GAGGCGGTACCGGTGCGCGTGAAGATGTTGAAAAGATGATGCCACAGAGAAACCTTTCT 1860
OY 1861 GATCTGTTGTGAGATGAGATGATGAAAGATGATTTGGGAAAACAAAGATATTCATAAT 1920
DB 1861 GATCTGTTGTGAGATGAGATGATGAAAGATGATTTGGGAAAACAAAGATATTCATAAT 1920
OY 1921 CTCTTGGAGCCTGACACAGAGATGGGCTCTCTATGTCTATGATGATGATGATGATGATGAT 1980
DB 1921 CTCTTGGAGCCTGACACAGAGATGGGCTCTCTATGTCTATGATGATGATGATGATGATGAT 1980
OY 1981 GGCACACCTCCAGAAATACCTCCGAGCCCGAGAGCCACCCCGGATGAGATCTCTATGAC 2040
DB 1981 GGCACACCTCCAGAAATACCTCCGAGCCCGAGAGCCACCCCGGATGAGATCTCTATGAC 2040
OY 2041 ATTAACGCTGTTCTGAGAGAGATGACCTTCAAGGACTTGGTGTCTATGACCTACAG 2100
DB 2041 ATTAACGCTGTTCTGAGAGAGATGACCTTCAAGGACTTGGTGTCTATGACCTACAG 2100
OY 2101 CTGGCCAGAGCAGTGAAGTACTTGGCTTCCAAAATATATTCATCGATTTAGACACC 2160
DB 2101 CTGGCCAGAGCAGTGAAGTACTTGGCTTCCAAAATATATTCATCGATTTAGACACC 2160
OY 2161 AGAATGTTTGGTGAACGAAACAAATGTGATGAAATAGACAGACTTTGGACCTGCCAGA 2220
DB 2161 AGAATGTTTGGTGAACGAAACAAATGTGATGAAATAGACAGACTTTGGACCTGCCAGA 2220

OY 2221 GATATCAACATATAGACTATTTACAAAAGACCACCAATGGCGGCTTCCAGTCAAGTGG 2280
DB 2221 GATATCAACATATAGACTATTTACAAAAGACCACCAATGGCGGCTTCCAGTCAAGTGG 2280
OY 2281 ATGGCTCCAGAACCCCTGTTTGTATAGATATACACTCATCAGAGTGAATGTCGTCTTC 2340
DB 2281 ATGGCTCCAGAACCCCTGTTTGTATAGATATACACTCATCAGAGTGAATGTCGTCTTC 2340
OY 2341 GGGGTGTATATGTGGAGATCTTCACTTTAGGGGCTCCGCCCTACCCAGAGATTCGGTG 2400
DB 2341 GGGGTGTATATGTGGAGATCTTCACTTTAGGGGCTCCGCCCTACCCAGAGATTCGGTG 2400
OY 2401 GAGGAACCTTTTAAGCTGTGAAGAGAGACACAGAAATGATTAAGCCAACTGACAC 2460
DB 2401 GAGGAACCTTTTAAGCTGTGAAGAGAGACACAGAAATGATTAAGCCAACTGACAC 2460
OY 2461 AAGGAACCTGATGATGATGATGAGGAGCTTTGGCATGACAGTCCCTCCAGAGACCAAG 2520
DB 2461 AAGGAACCTGATGATGATGATGAGGAGCTTTGGCATGACAGTCCCTCCAGAGACCAAG 2520
OY 2521 TTCAAGCACTTGGTGAAGAGACTTGGATGCAATTCCTACTCTCACAACCAATGAGAAATAC 2580
DB 2521 TTCAAGCACTTGGTGAAGAGACTTGGATGCAATTCCTACTCTCACAACCAATGAGAAATAC 2580
OY 2581 TTGAGACCTGAGCCCAACCTCTGAACAGTATTCACCTAGTTACCTGACACAAAGATTC 2640
DB 2581 TTGAGACCTGAGCCCAACCTCTGAACAGTATTCACCTAGTTACCTGACACAAAGATTC 2640
OY 2641 TGTCTTTCAGAGATGATTCGTTTCTCCAGACCCCATGCTCTTACGAACCATGCGCTT 2700
DB 2641 TGTCTTTCAGAGATGATTCGTTTCTCCAGACCCCATGCTCTTACGAACCATGCGCTT 2700
OY 2701 CCTCAGTATCCACATATAAGCGCAGTGTAAACATGATGATGATGATGATGATGATGATGAT 2760
DB 2701 CCTCAGTATCCACATATAAGCGCAGTGTAAACATGATGATGATGATGATGATGATGATGAT 2760
OY 2761 CAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGGGAGACCATGCGTCCAGAGC 2820
DB 2761 CAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGGGAGACCATGCGTCCAGAGC 2820
OY 2821 TTTGTTGTCTCCACTTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
DB 2821 TTTGTTGTCTCCACTTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
OY 2881 TATGTGTAAAGTTATATACAGTTGAAACTGTATCTTCCCGAGAGACAAAGAGTT 2940
DB 2881 TATGTGTAAAGTTATATACAGTTGAAACTGTATCTTCCCGAGAGACAAAGAGTT 2940
OY 2941 TCTGAGCAGTGGACTGCGACAAAGCCACATGTAAACCCCTCTCACTGCGGTCTG 3000
DB 2941 TCTGAGCAGTGGACTGCGACAAAGCCACATGTAAACCCCTCTCACTGCGGTCTG 3000
OY 3001 GCTGTGACAGTGAAGACTCAAGGTGAGCGTGTGCTTCCCTCTCTGTTAATTTGTAA 3060
DB 3001 GCTGTGACAGTGAAGACTCAAGGTGAGCGTGTGCTTCCCTCTCTGTTAATTTGTAA 3060
OY 3061 TAAATGAGAGATTTATGTAGACACACACTTACAGAGCCAAATGCAAGTATATAGTGC 3120
DB 3061 TAAATGAGAGATTTATGTAGACACACACTTACAGAGCCAAATGCAAGTATATAGTGC 3120
OY 3121 TGGATGATGTAATATATTCAAATTTATGTATATATATATATATATATATATATATATAT 3180
DB 3121 TGGATGATGTAATATATTCAAATTTATGTATATATATATATATATATATATATATATATAT 3180
OY 3181 TATTTTGTATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
DB 3181 TATTTTGTATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
OY 3241 TTTTAAATAGCTATTTGTAATATGCTGTCTTACACATATATTTCTTAAATTTTACACGGACA 3300
DB 3241 TTTTAAATAGCTATTTGTAATATGCTGTCTTACACATATATTTCTTAAATTTTACACGGACA 3300
OY 3301 GAGGTGAAAAAATACCTTTTGTGCTTCCAGGAAAAATGATTAACGTTAATTTAATTAAT 3360

|||||
 Db 3301 GAGGTGAGAAATACCTTTTGGCTTTAGGMAAATGCTAATGCTAATTTATATAT 3360
 |||||
 Oy 3361 TCGTATATACAAACAATTAATCATTTATAGTTTTTTTCTAAATTAAGTGCCATTTCT 3420
 |||||
 Db 3361 TCGTATATACAAACAATTAATCATTTATAGTTTTTTTCTAAATTAAGTGCCATTTCT 3420
 |||||
 Oy 3421 ATGCAGGAGCAGCAGCAGACTAGTAACTATGCTTGGACTTAACCTAGTATCGATCC 3480
 |||||
 Db 3421 ATGCAGGAGCAGCAGCAGACTAGTAACTATGCTTGGACTTAACCTAGTATCGATCC 3480
 |||||
 Oy 3481 TTTGAAAAGAGATATTTACATATATGACTAATTTGGGAAATGAGTTTGAATTA 3540
 |||||
 Db 3481 TTTGAAAAGAGATATTTACATATATGACTAATTTGGGAAATGAGTTTGAATTA 3540
 |||||
 Oy 3541 TTTGTTTAAATGCTGCTGCTGACAGGATTTCTTAAAGCTTCTAAATGCCATATTA 3600
 |||||
 Db 3541 TTTGTTTAAATGCTGCTGCTGACAGGATTTCTTAAAGCTTCTAAATGCCATATTA 3600
 |||||
 Oy 3601 AAGAACTCATTTATAGAAAGGTTTCAATTTGGTGTGCAACCCCTGCTAATACGTCACG 3660
 |||||
 Db 3601 AAGAACTCATTTATAGAAAGGTTTCAATTTGGTGTGCAACCCCTGCTAATACGTCACG 3660
 |||||
 Oy 3661 CAACGCTCACTGAGACTTCCCAAGATATGCTACAGGCTCTCTTAAAGATGCTTA 3720
 |||||
 Db 3661 CAACGCTCACTGAGACTTCCCAAGATATGCTACAGGCTCTCTTAAAGATGCTTA 3720
 |||||
 Oy 3721 ATCCATCTCTTGAAGCAGACACTTAAGTGAATGATAGCAGATGCTTCTCTGCGA 3780
 |||||
 Db 3721 ATCCATCTCTTGAAGCAGACACTTAAGTGAATGATAGCAGATGCTTCTCTGCGA 3780
 |||||
 Oy 3781 GCTGGCTTCTGCTGCTGCTGACATTAATCAGATTAAGCTGCTGCTGAGTGAAT 3840
 |||||
 Db 3781 GCTGGCTTCTGCTGCTGCTGACATTAATCAGATTAAGCTGCTGCTGAGTGAAT 3840
 |||||
 Oy 3841 TTTGATTAATGCTTCCAGACTTTTGGCTTGGAGACGCTGTTAGAGATCTTCAAGTCCA 3900
 |||||
 Db 3841 TTTGATTAATGCTTCCAGACTTTTGGCTTGGAGACGCTGTTAGAGATCTTCAAGTCCA 3900
 |||||
 Oy 3901 TCATTAAGAAATTTGAACACAGAGCTTTCTGCTGATAGTTTGGGATACGTCATCTTT 3960
 |||||
 Db 3901 TCATTAAGAAATTTGAACACAGAGCTTTCTGCTGATAGTTTGGGATACGTCATCTTT 3960
 |||||
 Oy 3961 TTTAAGGATTTGCTTATCATTAATTTGCGAGGACCTCACCAAAAGATCCAGCTCATACC 4020
 |||||
 Db 3961 TTTAAGGATTTGCTTATCATTAATTTGCGAGGACCTCACCAAAAGATCCAGCTCATACC 4020
 |||||
 Oy 4021 TACATCAGACAAATATCGCCGTTGCTTCTGTAATAAGTATGCTTTGCTTTGG 4080
 |||||
 Db 4021 TACATCAGACAAATATCGCCGTTGCTTCTGTAATAAGTATGCTTTGCTTTGG 4080
 |||||
 Oy 4081 AAACACCCACTCTCTTGGCAATAGCCGTCAGATGAGATGAGATACAGTCTTATG 4140
 |||||
 Db 4081 AAACACCCACTCTCTTGGCAATAGCCGTCAGATGAGATGAGATACAGTCTTATG 4140
 |||||
 Oy 4141 TGTTAACAAATTTGAGAAAGTATTTAATAAACCTTAAATTTTAACTAGCAATATAA 4200
 |||||
 Db 4141 TGTTAACAAATTTGAGAAAGTATTTAATAAACCTTAAATTTTAACTAGCAATATAA 4200
 |||||
 Oy 4201 ATGTTTCTACAGATTTAATGTTAACAAGACAAATTAATGTCAGCAACTTAAAAAAA 4260
 |||||
 Db 4201 ATGTTTCTACAGATTTAATGTTAACAAGACAAATTAATGTCAGCAACTTAAAAAAA 4260
 |||||
 Oy 4261 AAAAAAA 4268
 |||||
 Db 4261 AAAAAAA 4268
 |||||

XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:4626.
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytosolic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN M0200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PE 30-MAY-2001; 2001WO-US10838.
 XX
 PF 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI; 2002-188264/24.
 XX
 PT screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX
 PS Claim 1; SEQ ID 4626; 44pp; English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I1) of a signature gene set, where (I1)
CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664
CC to ABU70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I1) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 4268 BP: 1199 A; 964 C; 1028 G; 1077 T; 0 other:

Query Match 100.0%; Score 4268; DB 24; Length 4268;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGGACACACTCTTGTGCTTTGGAGTTGCTCCCAACACCCCGGCTCTGCTTTTC 60
DB 1 CCCAAGGACACACTCTTGTGCTTTGGAGTTGCTCCCAACACCCCGGCTCTGCTTTTC 60
QY 61 TCCATCCCGACCCACCGGGGGGGGGGACACACAGTGGCGGAGAGGCTTGCATTTC 120
DB 61 TCCATCCCGACCCACCGGGGGGGGGGACACACAGTGGCGGAGAGGCTTGCATTTC 120
QY 121 AAGTACTGACAGAGAGAGCGGAGCGGCTGCTGTTCTGAGCCCAACCGCAGGCTGAAGCA 180
DB 121 AAGTACTGACAGAGAGAGCGGAGCGGCTGCTGTTCTGAGCCCAACCGCAGGCTGAAGCA 180
QY 181 TTGCGGCTATCATGCTCCCTAGAGAGAGTGTGCAGATGGGATTAACTCCACATGGAGA 240
DB 181 TTGCGGCTATCATGCTCCCTAGAGAGAGTGTGCAGATGGGATTAACTCCACATGGAGA 240
QY 241 TATGAAGAGAGACCGGGGATTTGGTACCGTAAACATGGTGGGCTGTTTCATCTGC 300
DB 241 TATGAAGAGAGACCGGGGATTTGGTACCGTAAACATGGTGGGCTGTTTCATCTGC 300
QY 301 CTGCTGTGTGTCACCATGCGCAACCTTGTCCCTGCGCGGCTCTCTCAAGTTAGTTGAG 360
DB 301 CTGCTGTGTGTCACCATGCGCAACCTTGTCCCTGCGCGGCTCTCTCAAGTTAGTTGAG 360
QY 361 GATACACATTAAG 420
DB 361 GATACACATTAAG 420
QY 421 TACGTGGCTGCGGAG 480
DB 421 TACGTGGCTGCGGAG 480
QY 481 ATCAGTTGGACTAAG 540
DB 481 ATCAGTTGGACTAAG 540
QY 541 GAGTACTTGAGATAAG 600
DB 541 GAGTACTTGAGATAAG 600
QY 601 ACTAGAGACTGTAG 660
DB 601 ACTAGAGACTGTAG 660
QY 661 TCCGAG 720
DB 661 TCCGAG 720

QY 721 AACAGAGACACCATCTAGGACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 AACAGAGACACCATCTAGGACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 CTTGCGGACCAACTGTCAAGTTTCGCTGCCAGCGCGGGGAGAACCAATGCCAACCATG 840
DB 781 CTTGCGGACCAACTGTCAAGTTTCGCTGCCAGCGCGGGGAGAACCAATGCCAACCATG 840
QY 841 CCGTGGGTGAG 900
DB 841 CCGTGGGTGAG 900
QY 901 CGAAGCAGACTGAGACCTCATTTATGGAAGTGGTCCCATCTGACAGAGAGAGAGAG 960
DB 901 CGAAGCAGACTGAGACCTCATTTATGGAAGTGGTCCCATCTGACAGAGAGAGAGAG 960
QY 961 ACCGTGTGTGAG 1020
DB 961 ACCGTGTGTGAG 1020
QY 1021 GACCGATCGGCTCACCGGCGCCATCTCAAGCCGAGCTGCCGCAATGCTCCACAGTG 1080
DB 1021 GACCGATCGGCTCACCGGCGCCATCTCAAGCCGAGCTGCCGCAATGCTCCACAGTG 1080
QY 1081 GTGAGAGAGACGTAGAGTTGTCTGCAAGGTTTACAGTGAATGCCAGCCCATCCAG 1140
DB 1081 GTGAGAGAGACGTAGAGTTGTCTGCAAGGTTTACAGTGAATGCCAGCCCATCCAG 1140
QY 1141 TGGATCAAGCAGCTGAG 1200
DB 1141 TGGATCAAGCAGCTGAG 1200
QY 1201 AAGTTCTCAAGGCGCGCGCTGTTAAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 AAGTTCTCAAGGCGCGCGCTGTTAAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 CGGAAATGAACCTTTTAG 1320
DB 1261 CGGAAATGAACCTTTTAG 1320
QY 1321 ATATCTTTCACCTCTCATAGTTGTGACAGTTTCCAGCGGCTGGAAGAGAGAGAGAT 1380
DB 1321 ATATCTTTCACCTCTCATAGTTGTGACAGTTTCCAGCGGCTGGAAGAGAGAGAGAT 1380
QY 1381 ACAGCTTCCCGAGACACTGCGAGATAGGATTAAGGATCTTCTTAATCCGC 1440
DB 1381 ACAGCTTCCCGAGACACTGCGAGATAGGATTAAGGATCTTCTTAATCCGC 1440
QY 1441 TGTATGTTGTAACAGTCACTCTGTGCGAATGAAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 TGTATGTTGTAACAGTCACTCTGTGCGAATGAAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 AGCAGCAGCGCGCTGTGCAAGAGCTGACCAACAGTATCCCTGCGGAGAGAGATTA 1560
DB 1501 AGCAGCAGCGCGCTGTGCAAGAGCTGACCAACAGTATCCCTGCGGAGAGAGATTA 1560
QY 1561 GTTTCGGCTGAGTCCAGCTCTCTCATGAACTCAACACCCGCTGTGAGATTAACAA 1620
DB 1561 GTTTCGGCTGAGTCCAGCTCTCTCATGAACTCAACACCCGCTGTGAGATTAACAA 1620
QY 1621 GCGCTCTCTTCAACGAGCAGACACCCCATGCTGAGAGGGGTCTCCGAGATTAACCTT 1680
DB 1621 GCGCTCTCTTCAACGAGCAGACACCCCATGCTGAGAGGGGTCTCCGAGATTAACCTT 1680
QY 1681 GAGGAGCCCAAAATGGAGAGTTTCAAGAGATTAAGCTGACCTGCGCAAGCCCTG 1740
DB 1681 GAGGAGCCCAAAATGGAGAGTTTCAAGAGATTAAGCTGACCTGCGCAAGCCCTG 1740
QY 1741 GGTTCCTTTGGGCAAGTGTCTATGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 GGTTCCTTTGGGCAAGTGTCTATGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 GAGCGGCTACCGCTGCGCTGAAGATGTTGAAAGATGATGCCACAGAGAGAGAGAG 1860
DB 1801 GAGCGGCTACCGCTGCGCTGAAGATGTTGAAAGATGATGCCACAGAGAGAGAGAG 1860

```
Db 1801 GAGCGGTACCGTGGCCCTGAAAGATGTTGAAGATGATGCCACAGAGAAACCTTTCT 1860
|||
Qy 1861 GATTCGTGTCAGAGATGAGATGATGAAGATGATTGGGAAACACAAGAAATATCATAAAT 1920
|||
Db 1861 GATTCGTGTCAGAGATGAGATGATGAAGATGATTGGGAAACACAAGAAATATCATAAAT 1920
|||
Qy 1921 CTTCCTGGAGCCTGCACACAGATGGGCTCTCTATGTATAGTTGAGTATGCTCTTAA 1980
|||
Db 1921 CTTCCTGGAGCCTGCACACAGATGGGCTCTCTATGTATAGTTGAGTATGCTCTTAA 1980
|||
Qy 1981 GGCACCTCCGAGCAATACCTCCGAGCCGAGCCACCCGGATGAGTACTTCATGAC 2040
|||
Db 1981 GGCACCTCCGAGCAATACCTCCGAGCCGAGCCACCCGGATGAGTACTTCATGAC 2040
|||
Qy 2041 ATTAACCGTCTCTGAGGAGAGATGACCTTCAGCACTTGCTGTCATGACCTACGAG 2100
|||
Db 2041 ATTAACCGTCTCTGAGGAGAGATGACCTTCAGCACTTGCTGTCATGACCTACGAG 2100
|||
Qy 2101 CTGGCCAGAGGCAATGAGTATGCTGCCAAAATGTTATGATGAGATTTAGCAGCC 2160
|||
Db 2101 CTGGCCAGAGGCAATGAGTATGCTGCCAAAATGTTATGATGAGATTTAGCAGCC 2160
|||
Qy 2161 AGAAATGTTTGTAAACAGAAAACAAATGTGATGAAAATAGCAGACTTTGGACTGCCAGA 2220
|||
Db 2161 AGAAATGTTTGTAAACAGAAAACAAATGTGATGAAAATAGCAGACTTTGGACTGCCAGA 2220
|||
Qy 2221 GATATCAACATATATAGACTATTACAAAAGACACCAATGGGGGCTTCAGTCAAGTGG 2280
|||
Db 2221 GATATCAACATATATAGACTATTACAAAAGACACCAATGGGGGCTTCAGTCAAGTGG 2280
|||
Qy 2281 ATGGCTCCAGACAGCCCGTGTGATAGATATACATCATACAGATGATGCTGCTTC 2340
|||
Db 2281 ATGGCTCCAGACAGCCCGTGTGATAGATATACATCATACAGATGATGCTGCTTC 2340
|||
Qy 2341 GGGGTGTTAAATGTGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCGGTG 2400
|||
Db 2341 GGGGTGTTAAATGTGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCGGTG 2400
|||
Qy 2401 GAGGAACCTTTTAAAGCTGCGTAAGGAAGGACACAGAAATGATTAAGCAAGCAACTGCAC 2460
|||
Db 2401 GAGGAACCTTTTAAAGCTGCGTAAGGAAGGACACAGAAATGATTAAGCAAGCAACTGCAC 2460
|||
Qy 2461 AAGCACTGTACATGATGATGAGGAGACTGTTGGCATGCAATGCCCTCCAGAACCAAG 2520
|||
Db 2461 AAGCACTGTACATGATGATGAGGAGACTGTTGGCATGCAATGCCCTCCAGAACCAAG 2520
|||
Qy 2521 TTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCCTCAGTCTCACAAACCAATGAGGAATAC 2580
|||
Db 2521 TTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCCTCAGTCTCACAAACCAATGAGGAATAC 2580
|||
Qy 2581 TTGGACCTCAGCCAACTCTCGAAGCAATTCACCTAGTTACCTGACACAAAGTTCT 2640
|||
Db 2581 TTGGACCTCAGCCAACTCTCGAAGCAATTCACCTAGTTACCTGACACAAAGTTCT 2640
|||
Qy 2641 TGTCTTCAAGAGATGATCTGTTTTTCTCAGAGACCCCATGGCTTACGAACATGCTT 2700
|||
Db 2641 TGTCTTCAAGAGATGATCTGTTTTTCTCAGAGACCCCATGGCTTACGAACATGCTT 2700
|||
Qy 2701 CCTGAGTATGCACAGATTAAGCGCAGTGTAAAAACATGATGACTGTGTGCTGCC 2760
|||
Db 2701 CCTGAGTATGCACAGATTAAGCGCAGTGTAAAAACATGATGACTGTGTGCTGCC 2760
|||
Qy 2761 CAACAGAGACAGCTGGGAACCTAGCTACACTGAGCAGGAGACATGCTGCCAGAGC 2820
|||
Db 2761 CAACAGAGACAGCTGGGAACCTAGCTACACTGAGCAGGAGACATGCTGCCAGAGC 2820
|||
Qy 2821 TTGTTCTCTCCACTTGTATATATGATCAGAGAGTAAATTAATTTGAAAAATATCAGCA 2880
|||
Db 2821 TTGTTCTCTCCACTTGTATATATGATCAGAGAGTAAATTAATTTGAAAAATATCAGCA 2880
|||
Qy 2881 TATGTGAAGATTTATACAGTTGAAAACTTGTATCTTCCCGAGGAGAGAAAGTT 2940
|||
Db 2881 TATGTGAAGATTTATACAGTTGAAAACTTGTATCTTCCCGAGGAGAGAAAGTT 2940
|||

Db 2881 TATGTGAAGATTTATACAGTTGAAAACTTGTATCTTCCCGAGGAGAGAAAGTT 2940
|||
Qy 2941 TCTGAGCAGTGTGACTGCGCACAGCCACCATGTAAACCCCTCTCACACCTCGCTTCG 3000
|||
Db 2941 TCTGAGCAGTGTGACTGCGCACAGCCACCATGTAAACCCCTCTCACACCTCGCTTCG 3000
|||
Qy 3001 GCTGTGACCACTAGACATCAAGGTGACGTCGTTGCTCCCTGTTAATTTGTA 3060
|||
Db 3001 GCTGTGACCACTAGACATCAAGGTGACGTCGTTGCTCCCTGTTAATTTGTA 3060
|||
Qy 3061 TAATTGAGACAGATTTATGTCACACACTTACAGACACAAATGCAATATATAGTGC 3120
|||
Db 3061 TAATTGAGACAGATTTATGTCACACACTTACAGACACAAATGCAATATATAGTGC 3120
|||
Qy 3121 TGAATGATGATAATATATCAATTAATGATATATATATATATATATATATATATATAT 3180
|||
Db 3121 TGAATGATGATAATATATCAATTAATGATATATATATATATATATATATATATATATAT 3180
|||
Qy 3181 TATTTTGTATTTGATTTTAAATGATGTCGCCAATGCACTTGAATAATTTGCTCTTT 3240
|||
Db 3181 TATTTTGTATTTGATTTTAAATGATGTCGCCAATGCACTTGAATAATTTGCTCTTT 3240
|||
Qy 3241 TTTTATACCTATTGCTTAATGCTGTTCTTACACATAATTTCTTAATTTTACCGAGCA 3300
|||
Db 3241 TTTTATACCTATTGCTTAATGCTGTTCTTACACATAATTTCTTAATTTTACCGAGCA 3300
|||
Qy 3301 GAGGTGAAAAATATCTTTCCTTTCAGGAAAAATGATATACCTTAATTTATTAAT 3360
|||
Db 3301 GAGGTGAAAAATATCTTTCCTTTCAGGAAAAATGATATACCTTAATTTATTAAT 3360
|||
Qy 3361 TGGTAATATACAAAACAAATTAATCATTTATAGTTTTTTTGTAAATTAAGGCAATTC 3420
|||
Db 3361 TGGTAATATACAAAACAAATTAATCATTTATAGTTTTTTTGTAAATTAAGGCAATTC 3420
|||
Qy 3421 ATGCAGGACGACAGACAGACTATTAATCTATGCTTGGACCTACTATATATGATGC 3480
|||
Db 3421 ATGCAGGACGACAGACAGACTATTAATCTATGCTTGGACCTACTATATATGATGC 3480
|||
Qy 3481 TTTGAAGAAGAAATATTTCAATATATGACTAATTTGGGAAAAATGAACTTTGATTTAT 3540
|||
Db 3481 TTTGAAGAAGAAATATTTCAATATATGACTAATTTGGGAAAAATGAACTTTGATTTAT 3540
|||
Qy 3541 TTGTGTTAAATGCTGCTGTACAGCAATTTCTTAAGCTCTTAATGCCCCATATTAA 3600
|||
Db 3541 TTGTGTTAAATGCTGCTGTACAGCAATTTCTTAAGCTCTTAATGCCCCATATTAA 3600
|||
Qy 3601 AAGAACTCATCTATAGGAAGGTGTTCAATTTGGTGGCAACCTGCTATTAAGTCAAG 3660
|||
Db 3601 AAGAACTCATCTATAGGAAGGTGTTCAATTTGGTGGCAACCTGCTATTAAGTCAAG 3660
|||
Qy 3661 CAACGCTAAGTGTGACTTCCCAAGATAAATGATACAGGCTCCTTTAAAGATGCTTAA 3720
|||
Db 3661 CAACGCTAAGTGTGACTTCCCAAGATAAATGATACAGGCTCCTTTAAAGATGCTTAA 3720
|||
Qy 3721 ATTCATTTCTTGGAGACAGACCTTAACTTGAATATGATAGCAAGATGTGCTCTGGGA 3780
|||
Db 3721 ATTCATTTCTTGGAGACAGACCTTAACTTGAATATGATAGCAAGATGTGCTCTGGGA 3780
|||
Qy 3781 GCTGGCTTCTGCTTCTGAGTTGACATTAATCAGATTATAGCCTGATTTCTTCACTGAAT 3840
|||
Db 3781 GCTGGCTTCTGCTTCTGAGTTGACATTAATCAGATTATAGCCTGATTTCTTCACTGAAT 3840
|||
Qy 3841 TTTGATTAATGGCTTCCAGACTTTTGGTGTGAGAGCGCTGTTAAGATCTTCAAGTCCA 3900
|||
Db 3841 TTTGATTAATGGCTTCCAGACTTTTGGTGTGAGAGCGCTGTTAAGATCTTCAAGTCCA 3900
|||
Qy 3901 TCAATGAAAAATTAACACAGAGTTGTTCTGCTGATATGTTTGGGATATGCTCCATCTT 3960
|||
Db 3901 TCAATGAAAAATTAACACAGAGTTGTTCTGCTGATATGTTTGGGATATGCTCCATCTT 3960
|||
Qy 3961 TTAAGGATGCTTTCATCTAATTTGAGCAGACCTCACCAAAAAGATCCAGCCTCATACC 4020
|||
Db 3961 TTAAGGATGCTTTCATCTAATTTGAGCAGACCTCACCAAAAAGATCCAGCCTCATACC 4020
|||
```


Db 301 CTGGTCGTGGTCCCATGGCAACCTGTCTCCCTGGCCGCGCCCTCTTACGTTTAGTTGAG 360
Oy 361 GATACACATTAGAGCCAGAGAGCCACCAACCAATACCAATCTCTCAACAGAAAGTG 420
Db 361 GATACACATTAGAGCCAGAGAGCCACCAACCAATACCAATCTCTCAACAGAAAGTG 420
Oy 421 TACGTGCTGGCCAGGGGAGTCCGTAGAGTGGCTGCTCTGTGAAAGATGCCGCGTG 480
Db 421 TACGTGCTGGCCAGGGGAGTCCGTAGAGTGGCTGCTCTGTGAAAGATGCCGCGTG 480
Oy 481 ATCATTTGGAGTAAGGATGGGGTGACATTGGGGCCCAACATAGAGACAGTCTTATTTGG 540
Db 481 ATCATTTGGAGTAAGGATGGGGTGACATTGGGGCCCAACATAGAGACAGTCTTATTTGG 540
Oy 541 GAGTACTTGCAGATAAAGGGCGCCACGCCCTAGAGACTCCGGCTCTATGTCTTACTGCC 600
Db 541 GAGTACTTGCAGATAAAGGGCGCCACGCCCTAGAGACTCCGGCTCTATGTCTTACTGCC 600
Oy 601 AGTAGAGCTGTAGAGAGTGAACCTTGGTACTTCATGTGTGAATGTGCAGATGCCACTTCA 660
Db 601 AGTAGAGCTGTAGAGAGTGAACCTTGGTACTTCATGTGTGAATGTGCAGATGCCACTTCA 660
Oy 661 TCCGAGATGATGAGAGTACACCCGATGGTGGGGAAGATTTTGTCACTAGAGAACAGTAAC 720
Db 661 TCCGAGATGATGAGAGTACACCCGATGGTGGGGAAGATTTTGTCACTAGAGAACAGTAAC 720
Oy 721 AACAGAGAGACCACTACTGACCAACACAGAAAGATGGAAGACCGGCTCATCTCTGTG 780
Db 721 AACAGAGAGACCACTACTGACCAACACAGAAAGATGGAAGACCGGCTCATCTCTGTG 780
Oy 781 CTTGGGGGCAACACTGTCAAGTTTGGCTGCCACGCCGGGGGAGACCAATGGCCAAACATG 840
Db 781 CTTGGGGGCAACACTGTCAAGTTTGGCTGCCACGCCGGGGGAGACCAATGGCCAAACATG 840
Oy 841 CCGTGCGCTGAAAAAGCGGAGAGGTTTAAAGAGAGCATCGCATTTGGAGCGCTACAAGTA 900
Db 841 CCGTGCGCTGAAAAAGCGGAGAGGTTTAAAGAGAGCATCGCATTTGGAGCGCTACAAGTA 900
Oy 901 CGAAGACAGCACTGGAGGCTCATTTATGGAAGTGTGTCCCTCTGACAAAGGAATAT 960
Db 901 CGAAGACAGCACTGGAGGCTCATTTATGGAAGTGTGTCCCTCTGACAAAGGAATAT 960
Oy 961 ACCGTGTGTGGAGAAATACGGGTCATCAATCAACAGTACAGCTGTGATTTGTG 1020
Db 961 ACCGTGTGTGGAGAAATACGGGTCATCAATCAACAGTACAGCTGTGATTTGTG 1020
Oy 1021 GAGCGATCGCTCACCGGCCCATCTTCAAGCGGAGCTCCGGCAAAATGCTTCACAGTG 1080
Db 1021 GAGCGATCGCTCACCGGCCCATCTTCAAGCGGAGCTCCGGCAAAATGCTTCACAGTG 1080
Oy 1081 GTCCGGAGAGAGTGAAGTTTGTCTGCAAGGTTTACAGTATGCCACAGCCCAATCCAG 1140
Db 1081 GTCCGGAGAGAGTGAAGTTTGTCTGCAAGGTTTACAGTATGCCACAGCCCAATCCAG 1140
Oy 1141 TGGATCAACACAGCTGGAAAAAGAGCGCAGTAAATACGGGCGCGAGCGGCTGCCCTAAC 1200
Db 1141 TGGATCAACACAGCTGGAAAAAGAGCGCAGTAAATACGGGCGCGAGCGGCTGCCCTAAC 1200
Oy 1201 AAGGTTCTCAAGCGCGCGGTGTTAAACACACAGGCAAAAGATTGAGTTCTTATATT 1260
Db 1201 AAGGTTCTCAAGCGCGCGGTGTTAAACACACAGGCAAAAGATTGAGTTCTTATATT 1260
Oy 1261 CGGAATGTAAGTATGAGAGCGTGGGGAATATACGTGCTTGGCGGTAATTTCTATTTGG 1320
Db 1261 CGGAATGTAAGTATGAGAGCGTGGGGAATATACGTGCTTGGCGGTAATTTCTATTTGG 1320
Oy 1321 ATATCTTTTCACTCTCATGTGTGACAGTTCTGCCAGCGCTGGAGAGAAAAAGAGATT 1380
Db 1321 ATATCTTTTCACTCTCATGTGTGACAGTTCTGCCAGCGCTGGAGAGAAAAAGAGATT 1380
Oy 1381 ACAGCTTCCCGACAGTACCTGAGATAGCCATTACTGATAGGGGTCTTAAATCGCC 1440
Db 1381 ACAGCTTCCCGACAGTACCTGAGATAGCCATTACTGATAGGGGTCTTAAATCGCC 1440

Db 1381 ACAGCTTCCCGACAGTACCTGAGATAGCCATTACTGATAGGGGTCTTAAATCGCC 1440
Oy 1441 TGTATGTGTGTAGACAGTATCTCTGTGCCGAATGAAGAACAGCAAGAACCCAGACTTC 1500
Db 1441 TGTATGTGTGTAGACAGTATCTCTGTGCCGAATGAAGAACAGCAAGAACCCAGACTTC 1500
Oy 1501 AGCAGCCAGCGCGCTGTGCACAAAGCTGACCAAAAGCTATCCCTGGCGAGACAGTAA 1560
Db 1501 AGCAGCCAGCGCGCTGTGCACAAAGCTGACCAAAAGCTATCCCTGGCGAGACAGTAA 1560
Oy 1561 GTTTCGGCTGAGTCCAGCTCTCTCATGAACTCCAAACACCCCGCTGGTAGATTAACAA 1620
Db 1561 GTTTCGGCTGAGTCCAGCTCTCTCATGAACTCCAAACACCCCGCTGGTAGATTAACAA 1620
Oy 1621 CGCTCTCTTCAAGGAGACACCCCATGCTGGCAGGGGTCTCCGATGAACTTCCA 1680
Db 1621 CGCTCTCTTCAAGGAGACACCCCATGCTGGCAGGGGTCTCCGATGAACTTCCA 1680
Oy 1681 GAGAGCCCAAAATGGGAGTTTCCAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
Db 1681 GAGAGCCCAAAATGGGAGTTTCCAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
Oy 1741 GGTTCCTTTGGGCAAGTGTCTATGCGGAGACAGTGGGAATTGCAAAAGCAAGCCCAAG 1800
Db 1741 GGTTCCTTTGGGCAAGTGTCTATGCGGAGACAGTGGGAATTGCAAAAGCAAGCCCAAG 1800
Oy 1801 GAGGCGGTACCGTGGCGGTGAAGATGTTGAAGATGTGCACAGAGAAAGACCTTCT 1860
Db 1801 GAGGCGGTACCGTGGCGGTGAAGATGTTGAAGATGTGCACAGAGAAAGACCTTCT 1860
Oy 1861 GATCTGTGTGAGAGATGAGATGATGAAGATTTGGGAAACCAAGAAATATCATTAAT 1920
Db 1861 GATCTGTGTGAGAGATGAGATGATGAAGATTTGGGAAACCAAGAAATATCATTAAT 1920
Oy 1921 CTTCTGGAGGCTGCACACAGATGGGCTCTCTATGTCAATGTTGATGCTCTAAA 1980
Db 1921 CTTCTGGAGGCTGCACACAGATGGGCTCTCTATGTCAATGTTGATGCTCTAAA 1980
Oy 1981 GCGAAGCTCCGAGAAATACCTCCGAGCCCGAGCCACCCGGGATGGAGTACTCTATGAC 2040
Db 1981 GCGAAGCTCCGAGAAATACCTCCGAGCCCGAGCCACCCGGGATGGAGTACTCTATGAC 2040
Oy 2041 ATTAACGCTGTTCTGAGAGACAGATGACCTTCAAGCACTTGGTGTCTACCTACCAG 2100
Db 2041 ATTAACGCTGTTCTGAGAGACAGATGACCTTCAAGCACTTGGTGTCTACCTACCAG 2100
Oy 2101 CTGGCCAGAGGAGTGAATGATCTGGCTTCCCAAAATGATTTCAATCGAGTTTAGCAGCC 2160
Db 2101 CTGGCCAGAGGAGTGAATGATCTGGCTTCCCAAAATGATTTCAATCGAGTTTAGCAGCC 2160
Oy 2161 AGAAATGTTTGGTAAACAGAAACAAATGTGAATAGCAGACTTGTGACTGCCAGA 2220
Db 2161 AGAAATGTTTGGTAAACAGAAACAAATGTGAATAGCAGACTTGTGACTGCCAGA 2220
Oy 2221 GATATCAACAATATAGCTATTTACAAAAAGACCAACATGGCGGCTTCCAGTCAAGTG 2280
Db 2221 GATATCAACAATATAGCTATTTACAAAAAGACCAACATGGCGGCTTCCAGTCAAGTG 2280
Oy 2281 ATGGCTCAGAAAGCCCTGTTGATAGAGTATCACTCATGAGAGTGTGTGGGCTTTC 2340
Db 2281 ATGGCTCAGAAAGCCCTGTTGATAGAGTATCACTCATGAGAGTGTGTGGGCTTTC 2340
Oy 2341 GGGGTGTATATGTGGAGATCTTCACTTATAGGGGCTGCCCTACCGAGGATTTCCCGTG 2400
Db 2341 GGGGTGTATATGTGGAGATCTTCACTTATAGGGGCTGCCCTACCGAGGATTTCCCGTG 2400
Oy 2401 GAGGAACCTTTTAACTGCTGAAGAGACACAGATGATTAAGCCAGCCAACTGCACC 2460
Db 2401 GAGGAACCTTTTAACTGCTGAAGAGACACAGATGATTAAGCCAGCCAACTGCACC 2460
Oy 2461 AACGAATGTATATGATGATGAGGAGCTGTTGGCATGAGAGTCCCTCCAGAGACCAAG 2520
Db 2461 AACGAATGTATATGATGATGAGGAGCTGTTGGCATGAGAGTCCCTCCAGAGACCAAG 2520

QY 2521 TTCAAGCAGTTGTTAGAGAGCTTGATTCGAATTTCTCACTCTCACAACCAATGAGAAATAC 2580
 DB 2522 TTCAAGCAGTTGTTAGAGAGCTTGATTCGAATTTCTCACTCTCACAACCAATGAGAAATAC 2580
 QY 2581 TTGGACCTCAGCAGCAGCTCTCGACAGATTTACCTAGTTACCTGACACCAAGAACTTCT 2640
 DB 2581 TTGGACCTCAGCAGCAGCTCTCGACAGATTTACCTAGTTACCTGACACCAAGAACTTCT 2640
 QY 2641 TGTCTTTCAGAGATGATTTCTGTTTTTCTCCGAGACCCCATGCTTACGAACCATGCTT 2700
 DB 2641 TGTCTTTCAGAGATGATTTCTGTTTTTCTCCGAGACCCCATGCTTACGAACCATGCTT 2700
 QY 2701 CCTCACTATCCACATTAACGCGCAGCTTTAAACATGATGACTGCTGCTGCTGCC 2760
 DB 2701 CCTCACTATCCACATTAACGCGCAGCTTTAAACATGATGACTGCTGCTGCTGCC 2760
 QY 2761 CAAACGAGCAGCAGCAGCAGCAGCTTACCTGACGAGCAGAGACCATGCTGCCAGAGC 2820
 DB 2761 CAAACGAGCAGCAGCAGCAGCAGCTTACCTGACGAGCAGAGACCATGCTGCCAGAGC 2820
 QY 2821 TTGTTGCTCCACTGTTATATATGATTCAGAGAGATTAATTTGGAAGAAATATCAGCA 2880
 DB 2821 TTGTTGCTCCACTGTTATATATGATTCAGAGAGATTAATTTGGAAGAAATATCAGCA 2880
 QY 2881 TATGCTTAAAGATTTTATACAGTTGAAACCTTGTATCTTCCGAGAGAGAGAAAGCTT 2940
 DB 2881 TATGCTTAAAGATTTTATACAGTTGAAACCTTGTATCTTCCGAGAGAGAGAAAGCTT 2940
 QY 2941 TCTGGAGCAGTGGAGCTGCGCACAAAGCCACATTAACCCCTCCAGCTGCCGCTGCTG 3000
 DB 2941 TCTGGAGCAGTGGAGCTGCGCACAAAGCCACATTAACCCCTCCAGCTGCCGCTGCTG 3000
 QY 3001 GCTGTGAGCAGTGGAGCTGCGCACAAAGCCACATTAACCCCTCCAGCTGCCGCTGCTG 3060
 DB 3001 GCTGTGAGCAGTGGAGCTGCGCACAAAGCCACATTAACCCCTCCAGCTGCCGCTGCTG 3060
 QY 3061 TAAATGGAGAAATTTATGTCACGACACCTTACAGAGCACAATGACAGTATATAGTGC 3120
 DB 3061 TAAATGGAGAAATTTATGTCACGACACCTTACAGAGCACAATGACAGTATATAGTGC 3120
 QY 3121 TGGATGTATGTAAATATATCAAAATTTATGATTAATATATATATATATATATATATAT 3180
 DB 3121 TGGATGTATGTAAATATATCAAAATTTATGATTAATATATATATATATATATATATAT 3180
 QY 3181 TATTTTGTATGTATTTTAAATGATGCCAATGCACTGAGAAATTTGCTCTCTT 3240
 DB 3181 TATTTTGTATGTATTTTAAATGATGCCAATGCACTGAGAAATTTGCTCTCTT 3240
 QY 3241 TTTTAAATGCTATTTTGTCTAAATGCTGCTTACACATTAATTTCTTAATTTTCACCGAGCA 3300
 DB 3241 TTTTAAATGCTATTTTGTCTAAATGCTGCTTACACATTAATTTCTTAATTTTCACCGAGCA 3300
 QY 3301 GAGGTGAGAAATTTCTTTGCTTTCAGGAGAAATGCTAATGCTAATTTTATATATAT 3360
 DB 3301 GAGGTGAGAAATTTCTTTGCTTTCAGGAGAAATGCTAATGCTAATTTTATATATAT 3360
 QY 3361 TGTATATATACAAAACAATTAATCAATTTATAGTTTTTTTGTATATTTAAGTGCATTTCT 3420
 DB 3361 TGTATATATACAAAACAATTAATCAATTTATAGTTTTTTTGTATATTTAAGTGCATTTCT 3420
 QY 3421 ATGCGAGCAGCAGCAGCAGCAGTAAATCTATGCTTGGAGCTTAATCTAGTATCAGATCC 3480
 DB 3421 ATGCGAGCAGCAGCAGCAGCAGTAAATCTATGCTTGGAGCTTAATCTAGTATCAGATCC 3480
 QY 3481 TTTGAGAAAGAAATATTTACATATATGCTAATTTGGGAGAAATGAGTTTGTATAT 3540
 DB 3481 TTTGAGAAAGAAATATTTACATATATGCTAATTTGGGAGAAATGAGTTTGTATATAT 3540
 QY 3541 TTGCTTTAAATGCTGCTGCTGACAGAGATTTCTTACAGCTTCAATATGCCCCATATTTAA 3600
 DB 3541 TTGCTTTAAATGCTGCTGCTGACAGAGATTTCTTACAGCTTCAATATGCCCCATATTTAA 3600

QY 3601 AAGAACTATTCATAGGAGAGTGTTCATTTTGGTGTGACACCTGTCTATTACGTCAACG 3660
 DB 3601 AAGAACTATTCATAGGAGAGTGTTCATTTTGGTGTGACACCTGTCTATTACGTCAACG 3660
 QY 3661 CAACGCTTACTGAGCTTCCCAAGATTAATGTTACAGAGCTCCTTTAAACATGCTTTA 3720
 DB 3661 CAACGCTTACTGAGCTTCCCAAGATTAATGTTACAGAGCTCCTTTAAACATGCTTTA 3720
 QY 3721 ATTCATTCCTTGAAGACAGACCTTAAGTTGAAATGATTAAGCAATGCTGCTCTGCA 3780
 DB 3721 ATTCATTCCTTGAAGACAGACCTTAAGTTGAAATGATTAAGCAATGCTGCTCTGCA 3780
 QY 3781 GCTGGCTTCTGCTCTGATGCTGACATTAATCAATTAATGCTGATTTCTTCACTGAT 3840
 DB 3781 GCTGGCTTCTGCTCTGATGCTGACATTAATCAATTAATGCTGATTTCTTCACTGAT 3840
 QY 3841 TTTGATTAATGCTTCCAGACTTTTGCCTTGGAGAGCCTGTAGAGATCTTCAAGTCCCA 3900
 DB 3841 TTTGATTAATGCTTCCAGACTTTTGCCTTGGAGAGCCTGTAGAGATCTTCAAGTCCCA 3900
 QY 3901 TCATAGAAATTTGAAACACAGAGTTGTTCTGCTGATAGTTTGGGGATACGTCAATCTT 3960
 DB 3901 TCATAGAAATTTGAAACACAGAGTTGTTCTGCTGATAGTTTGGGGATACGTCAATCTT 3960
 QY 3961 TTAAGGATGCTTTCATCTAATTTCTGAGAGACCTCAACAAATATCCAGCTTATACC 4020
 DB 3961 TTAAGGATGCTTTCATCTAATTTCTGAGAGACCTCAACAAATATCCAGCTTATACC 4020
 QY 4021 TACATCAGACAAATATATGCGCTTGTCTCTGCTGATTAAGATTTGTTTGGCTTTGG 4080
 DB 4021 TACATCAGACAAATATATGCGCTTGTCTCTGCTGATTAAGATTTGTTTGGCTTTGG 4080
 QY 4081 AAACACCCACTCTCTTTCATATAGCCGTGCAAGATGAATGCAAGATTAACAGTATATG 4140
 DB 4081 AAACACCCACTCTCTTTCATATAGCCGTGCAAGATGAATGCAAGATTAACAGTATATG 4140
 QY 4141 TGTTCAAAAATTTGGAAGATTAATTAATAACCGTTAATTTTATCTGACATATAA 4200
 DB 4141 TGTTCAAAAATTTGGAAGATTAATTAATAACCGTTAATTTTATCTGACATATAA 4200
 QY 4201 ATGTTTCTACAGATTTAATGTTTAAACAAGCAAAATTAATGTCACGCACTTAAAAAAA 4260
 DB 4201 ATGTTTCTACAGATTTAATGTTTAAACAAGCAAAATTAATGTCACGCACTTAAAAAAA 4260
 QY 4261 AAAAAAAA 4268
 DB 4261 AAAAAAAA 4268
 RESULT 4
 ID AAQ21004 standard; cDNA: 3416 BP.
 XX AAQ21004:
 AC 20-MAY-1992 (first entry)
 DT
 DE bek receptor protein gene.
 XX
 KW F13problast growth factor receptor; heparin binding proteins;
 XX tyrosine kinase; bacterially expressed kinase; CSF-1; PDGF; ss.
 OS Homo sapiens.
 OS
 FH
 FT Key Location/Qualifiers
 FT CDS 87..2546
 FT /*lag- a
 FT /product= bek receptor protein
 PN W09200999-A.
 XX
 PD 23-JAN-1992.
 XX

PF 03-JUL-1991: 91MO-US04745.
XX
XX 06-JUL-1990: 90US-0549587.
XX
XX (RORE) RORER INT HOLDINGS.
XX
PI Dione CA, Crumley G, Jeye MC, Schlessinger J;
XX
XX WPI: 1992-056827/07.
DR P-PSDB: AAR20750.
XX
XX New fibroblast growth factor receptor proteins - useful in
PT treating GF-mediated conditions e.g. angiogenesis of tumours,
PT mitogenic effects in psoriasis, arthritis
XX
XX Claim 11: Fig 8: 65pp; English.
XX
XX The cdna sequence was obtd. by screening a one day old human brain
CC stem cDNA library in lambda g11 with an antisense 33 base oligomer
CC (3 mbex) complementary to the 3' end of the murine bek coding sequence
CC (Kornbluth et al., Mol. Cell Biol. 8: 5541-5544), and using the
CC resultant clone, lambda bek5 to rescreen the library. NIH 3T3
CC cells were cotransfected with a 1:20 mixture of pSV2neo and the
CC bek expression vector conq. the bek probe inserted into pM30
CC immediately downstream of the SV40 promoter and cytomegalovirus
CC enhancer. Clones of bek transfected cells have increased binding
CC for afep receptors, the best being clone NbeKb which was used for
CC DNA sequencing. Receptor proteins encoded by this cdna sequence may
CC be used in pharmaceutical compsns. to inhibit undesirable heparin-
CC binding growth factor mediated cellular responses or to inhibit the
CC binding of an opportunistic pathogen to human cells. Such undesirable
CC responses may be growth factor stimulated angiogenesis and vascular-
CC isation of tumours, mitogenic effects in psoriasis, arthritis,
CC atherosclerosis and benign prostatic hypertrophy. The derived bek
CC protein may also be used for screening drugs.
XX See also AA021003, AA023618-20..
XX
XX Sequence 3416 BP: 953 A; 778 C; 868 G; 815 T; 2 other:
SQ

Query Match 79.2%; Score 3381; DB 13; Length 3416;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3406; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

93 CACAGGTCCGGGAGGAGCTTGCCATTCAAGTACGTGACGACGACGCGCGCTCG 152
Db 2 CCGAGTCCCGGAGGAGCTTGCCATTCAAGTACGTGACGACGACGCGCGCTCG 60
OY 153 TTCTGAGCCCAACCGGAGCTGAGGCGCTGAGTGCATGCGCGTAGAGGAAGTGT 212
Db 61 TTCTGAGCCCAACCGGAGCTGAGGCGCTGAGTGCATGCGCGTAGAGGAAGTGT 119
OY 213 GCAGATGGGATTAAGTCCATGCATGAGATGGAAGAGACCGGGATGTTGTAAC 272
Db 120 GCAGATGGGATTAAGTCCATGCATGAGATGGAAGAGACCGGGATGTTGTAAC 179
OY 273 CATGTCAGTGGGGGCGTTTCACTGCGGTGCTGTCACCATGGCAACCTTGCCT 332
Db 180 CATGTCAGTGGGGGCGTTTCACTGCGGTGCTGTCACCATGGCAACCTTGCCT 239
OY 333 GGGCGGCGCTCTCTTCAAGTTAAGTATGAGATACACATTAGAGCCGAAAGCCACCAAC 392
Db 240 GGGCGGCGCTCTCTTCAAGTTAAGTATGAGATACACATTAGAGCCGAAAGCCACCAAC 299
OY 393 CAATATCAAAATCTTCAACACAGAGTGAAGTGGCTGCCCGGAGGAGTCCGTAAAGT 452
Db 300 CAATATCAAAATCTTCAACACAGAGTGAAGTGGCTGCCCGGAGGAGTCCGTAAAGT 359
OY 453 GCGCTGCGTGTAAAGATGCGCGGTGATGATGAGTAAAGATGGGGTCACTTGGG 512
Db 360 GCGCTGCGTGTAAAGATGCGCGGTGATGATGAGTAAAGATGGGGTCACTTGGG 419
OY 513 GCCCAACAATAGAGAGTGTATTGGGAGTACTTGACAGATAAAGGGCGCCAGCCTAG 572
Db

Db 420 GCCCAACAATAGAGAGTGTATTGGGAGTACTTGACAGATAAAGGGCGCCAGCCTAG 479
OY 573 AGACTCCGGGCTCTATCTGTACTGCCACTAGACCTGTAGACGTAACCTGGTACTT 632
Db 480 AGACTCCGGGCTCTATCTGTACTGCCACTAGACCTGTAGACGTAACCTGGTACTT 539
OY 633 CATGTGAATGTCAAGATGCGCATCTCCGAGATGATGAGATGACACCGATGGTGC 692
Db 540 CATGTGAATGTCAAGATGCGCATCTCCGAGATGATGAGATGACACCGATGGTGC 599
OY 693 GGAAGATTTTGTCAGTAGAGAACTAACAACAGAGACACCATCTGACCAACAGAGA 752
Db 600 GGAAGATTTTGTCAGTAGAGAACTAACAACAGAGACACCATCTGACCAACAGAGA 659
OY 753 AAAGATGAAAGGGGCTCCATGCTGCGCGGGCCCAACACTGTCAAGTTTGGCTGCC 812
Db 660 AAAGATGAAAGGGGCTCCATGCTGCGCGGGCCCAACACTGTCAAGTTTGGCTGCC 719
OY 813 AGCGGGGGGAAACCAATGCCAACCATTCGGGTGCTGAAAAACGGGAAGAGTTTAAAGA 872
Db 720 AGCGGGGGGAAACCAATGCCAACCATTCGGGTGCTGAAAAACGGGAAGAGTTTAAAGA 779
OY 873 GGAGCATGCAATTGGAGGCTACAAAGTACGAACACGACCTGACGCTCATTTAGAAAG 932
Db 780 GGAGCATGCAATTGGAGGCTACAAAGTACGAACACGACCTGACGCTCATTTAGAAAG 839
OY 933 TGTGTCCTCATCTGACAAGGGAATTAATACCTGTGTGTGAGATGAATACGGTCCAT 992
Db 840 TGTGTCCTCATCTGACAAGGGAATTAATACCTGTGTGTGAGATGAATACGGTCCAT 899
OY 993 CAATACACGTAACCACTGTGATGTTGTGGAGCGATTCGCTCCACCGGCCATCTCAAGC 1052
Db 900 CAATACACGTAACCACTGTGATGTTGTGGAGCGATTCGCTCCACCGGCCATCTCAAGC 959
OY 1053 CGGACTCGCGGCAAAATGCTCTCACAGTGTGTGGAGAGAGCTAAGATTGTTCTGCAAGT 1112
Db 960 CGGACTCGCGGCAAAATGCTCTCACAGTGTGTGGAGAGAGCTAAGATTGTTCTGCAAGT 1019
OY 1113 TTACAGTATGGCCGAGCCCAACATCCAGTGGATCAAGCAGCTGGAAGAGAGCAGTAA 1172
Db 1020 TTACAGTATGGCCGAGCCCAACATCCAGTGGATCAAGCAGCTGGAAGAGAGCAGTAA 1079
OY 1173 ATACGGGCGCGAGGAGTGCCTTACCTCAAGTTCACAAGCCGCGGCTTTAACACCAC 1232
Db 1080 ATACGGGCGCGAGGAGTGCCTTACCTCAAGTTCACAAGCCGCGGCTTTAACACCAC 1139
OY 1233 GGACAAAGAGATTGAGTTCCTATATTGCGAATGTAACTTTTGAAGAGCGCTGGGAAFTA 1292
Db 1140 GGACAAAGAGATTGAGTTCCTATATTGCGAATGTAACTTTTGAAGAGCGCTGGGAAFTA 1199
OY 1293 TACGTGCTTGGGCGGTAATTATTTGAGATATCTTTCACTGTCGATGGTGAAGTTCT 1352
Db 1200 TACGTGCTTGGGCGGTAATTATTTGAGATATCTTTCACTGTCGATGGTGAAGTTCT 1259
OY 1353 GCCAGCGCTGGAAGAGAAAGAGATTAACAGCTTCCACAGTACCTGGAGATAGCCAT 1412
Db 1260 GCCAGCGCTGGAAGAGAAAGAGATTAACAGCTTCCACAGTACCTGGAGATAGCCAT 1319
OY 1413 TTACTGCAATAGGGGCTCTTAAATGCGCTGTATGTTGTAACAGATCATCTGTGCCAAT 1472
Db 1320 TTACTGCAATAGGGGCTCTTAAATGCGCTGTATGTTGTAACAGATCATCTGTGCCAAT 1379
OY 1473 GAAGAACACGACCAAGAACCCAGACTTCGACGAGCCGCGCTGTGCAACAGCTAGCCAA 1532
Db 1380 GAAGAACACGACCAAGAACCCAGACTTCGACGAGCCGCGCTGTGCAACAGCTAGCCAA 1439
OY 1533 ACGTATCCCTCTGCGAGAGACAGTAAACAGTTTCGGCTGAGTCAAGCTCTCCATGAACCTC 1592
Db 1440 ACGTATCCCTCTGCGAGAGACAGTAAACAGTTTCGGCTGAGTCAAGCTCTCCATGAACCTC 1499
OY 1593 CAACACCCCGCTGCTGTGAGATTAACAACACGCTCTTCAACGGAGACACCCCATGCT 1652
Db 1500 CAACACCCCGCTGCTGTGAGATTAACAACACGCTCTTCAACGGAGACACCCCATGCT 1559

QY 1653 GCGAGGGGTCGCGAGTATGAACCTCCAGAGACCCAAAAATGGAGTTTCCAGAGATTA 1712
DB 1560 GGGAGGGGTCGCGAGTATGAACCTCCAGAGACCCAAAAATGGAGTTTCCAGAGATTA 1619
QY 1713 GCGAGACTGCGGAAACCCCTGGGAGAGGTGCTTTGGCAAGTGTCTATGCGCGAAGC 1772
DB 1620 GCGAGACTGCGGAAACCCCTGGGAGAGGTGCTTTGGCAAGTGTCTATGCGCGAAGC 1679
QY 1773 AGTGGAAATTCAGAAAGACAAAGGCCCAAGAGGGGCTCAGCCGTGGCGTGAAGTGTGA 1832
DB 1680 AGTGGAAATTCAGAAAGACAAAGGCCCAAGAGGGGCTCAGCCGTGGCGTGAAGTGTGA 1739
QY 1833 AGATGATGCCACAGAGAAAGACCTTCTGATCTGTCTGAGAGATGAGATGTAAGAT 1892
DB 1740 AGATGATGCCACAGAGAAAGACCTTCTGATCTGTCTGAGAGATGAGATGTAAGAT 1799
QY 1893 GATTGGAAACCAAAATATCTAAATCTTCTTGAGACCTGCACACAGAGATGGCCCTCT 1952
DB 1800 GATTGGAAACCAAAATATCTAAATCTTCTTGAGACCTGCACACAGAGATGGCCCTCT 1859
QY 1953 CTATGTCATAGTTGATGATGCTCTCTAAAGCAACCTCCGAAATACCTCGAGCCGGAG 2012
DB 1860 CTATGTCATAGTTGATGATGCTCTCTAAAGCAACCTCCGAAATACCTCGAGCCGGAG 1919
QY 2013 GCCACCCGGAGTGAAGTACTCTATGACATTAACCGTGTCTGAGAGAGATGACCTT 2072
DB 1920 GCCACCCGGAGTGAAGTACTCTCTATGACATTAACCGTGTCTGAGAGAGATGACCTT 1979
QY 2073 CAAGGACTGGGTGTCATGACACCTACAGCTGGCCAGAGCATGAGTACTGTGCTTCCA 2132
DB 1980 CAAGGACTGGGTGTCATGACACCTACAGCTGGCCAGAGCATGAGTACTGTGCTTCCA 2039
QY 2133 AAAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2192
DB 2040 AAAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
QY 2193 GAAATATGACAGATTTGGAGCTGCGCAGAGATATCAACAATATGACTATTACAAAAAGAC 2252
DB 2100 GAAATATGACAGATTTGGAGCTGCGCAGAGATATCAACAATATGACTATTACAAAAAGAC 2159
QY 2253 CAGCAATGGGCGGCTTCCAGTCAAGTGAAGTGGTCCAGAGCCCTGTTGATGATGATTA 2312
DB 2160 CAGCAATGGGCGGCTTCCAGTCAAGTGAAGTGGTCCAGAGCCCTGTTGATGATGATTA 2219
QY 2313 CACTCATCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2372
DB 2220 CACTCATCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2279
QY 2373 GGGCTGCGGCTTCCAGGAGATTCGGTGAAGCACTTTTAAAGCTGCTGAAGAGACGA 2432
DB 2280 GGGCTGCGGCTTCCAGGAGATTCGGTGAAGCACTTTTAAAGCTGCTGAAGAGACGA 2339
QY 2433 CAGAATGATTAAGCCAGCACTGACCAAGCAAGTGTATGATGATGATGATGATGATGAT 2492
DB 2340 CAGAATGATTAAGCCAGCACTGACCAAGCAAGTGTATGATGATGATGATGATGATGAT 2399
QY 2493 GCATGCACTGCTCCAGAGACCAAGCTTCAAGCAGTTGATGAAGACTTGGATGCAAT 2552
DB 2400 GCATGCACTGCTCCAGAGACCAAGCTTCAAGCAGTTGATGAAGACTTGGATGCAAT 2459
QY 2553 TCTGACTCTCACAACCAATGAGGAATACTTGAACCTCAGCAACCTCTGAAACAGTATTC 2612
DB 2460 TCTGACTCTCACAACCAATGAGGAATACTTGAACCTCAGCAACCTCTGAAACAGTATTC 2519
QY 2613 ACCTAGTTACCTGACACAAAGATCTTGTCTTCAAGAGATGATGATGATGATGATGATGAT 2672
DB 2520 ACCTAGTTACCTGACACAAAGATCTTGTCTTCAAGAGATGATGATGATGATGATGATGAT 2579
QY 2673 AGACCCCATGCTTACGAACATGCTTCTCAGATATCACAACATTAACGGCAGTGTAA 2732
DB 2580 AGACCCCATGCTTACGAACATGCTTCTCAGATATCACAACATTAACGGCAGTGTAA 2639

QY 2733 AACATGATGACTGTGTCTGCTGCTGCTGCCCAACAGAGACGACTGGGAACCTGATAC 2792
DB 2640 AACATGATGACTGTGTCTGCTGCTGCTGCCCAACAGAGACGACTGGGAACCTGATAC 2699
QY 2793 TGAGCAGGGAGACCAATGCTCCAGAGCTTGTGTCTCAGCTTGTATATGATGATCAG 2852
DB 2700 TGAGCAGGGAGACCAATGCTCCAGAGCTTGTGTCTCAGCTTGTATATGATGATCAG 2759
QY 2853 GACTAAATATTTGGAAGATATCAGCATATGCTTAAAGATTATATCAGTTGAAACTTG 2912
DB 2760 GACTAAATATTTGGAAGATATCAGCATATGCTTAAAGATTATATCAGTTGAAACTTG 2819
QY 2913 TAATCTTCCAGAGAGAGAGAGAGAGTTTCTGAGCAGTGGAGCTGCCAGACCAATG 2972
DB 2820 TAATCTTCCAGAGAGAGAGAGAGTTTCTGAGCAGTGGAGCTGCCAGACCAATG 2879
QY 2973 TAAACCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3032
DB 2880 TAAACCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
QY 3033 CGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3092
DB 2940 CGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2999
QY 3093 ACAGACCAAAATGACAGTATATAGTGTGATGATGATGATGATGATGATGATGATGAT 3152
DB 3000 ACAGACCAAAATGACAGTATATAGTGTGATGATGATGATGATGATGATGATGATGAT 3059
QY 3153 AAAT 3212
DB 3060 AAAT 3119
QY 3213 AATGACCTAGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3272
DB 3120 AATGACCTAGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3179
QY 3273 CACATATATTTCTTAATTTTACCGAGCAGAGGTGCAAAATCTTTGCTTCAGGAAA 3332
DB 3180 CACATATATTTCTTAATTTTACCGAGCAGAGGTGCAAAATCTTTGCTTCAGGAAA 3239
QY 3333 ATGATATACGTTAATTTTATATATATATATATATATATATATATATATATATATAT 3392
DB 3240 ATGATATACGTTAATTTTATATATATATATATATATATATATATATATATATATAT 3299
QY 3393 TTTTCTTGAATTTAAGTGGCATTTCTATGACAGCAGACGACGACTGATATCTAT 3452
DB 3300 TTTTCTTGAATTTAAGTGGCATTTCTATGACAGCAGACGACGACTGATATCTAT 3359
QY 3453 TCGTTGGACTTAAGTAT 3509
DB 3360 TCGTTGGACTTAAGTAT 3416

RESULT 5
ABL61834
ID ABL61834 standard; DNA; 3244 BP.
XX ABL61834;
XX
DE 15-MAY-2002 (first entry)
XX
XX Colon adenocarcinoma related gene sequence SEQ ID NO:171.
XX
XX Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; anliumour; cancerous;
KM cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
OS Homo sapiens.
XX
XX W0200194629-A2.
XX
XX
PD 13-DEC-2001.

XX 30-MAY-2001: 2001WO-US10838.
 XX 05-JUN-2000: 2000US-209473P.
 PR 05-JUN-2000: 2000US-209531P.
 PR 18-SEP-2000: 2000US-233133P.
 PR 18-SEP-2000: 2000US-233617P.
 PR 20-SEP-2000: 2000US-234009P.
 PR 20-SEP-2000: 2000US-234034P.
 PR 20-SEP-2000: 2000US-234052P.
 PR 22-SEP-2000: 2000US-234509P.
 PR 22-SEP-2000: 2000US-234567P.
 PR 25-SEP-2000: 2000US-234923P.
 PR 25-SEP-2000: 2000US-234924P.
 PR 25-SEP-2000: 2000US-235077P.
 PR 25-SEP-2000: 2000US-235082P.
 PR 25-SEP-2000: 2000US-235134P.
 PR 25-SEP-2000: 2000US-235280P.
 PR 26-SEP-2000: 2000US-235637P.
 PR 26-SEP-2000: 2000US-235638P.
 PR 27-SEP-2000: 2000US-235711P.
 PR 27-SEP-2000: 2000US-235720P.
 PR 27-SEP-2000: 2000US-235840P.
 PR 27-SEP-2000: 2000US-235863P.
 PR 28-SEP-2000: 2000US-236028P.
 PR 28-SEP-2000: 2000US-236032P.
 PR 28-SEP-2000: 2000US-236033P.
 PR 28-SEP-2000: 2000US-236034P.
 PR 28-SEP-2000: 2000US-236109P.
 PR 28-SEP-2000: 2000US-236111P.
 PR 29-SEP-2000: 2000US-236842P.
 PR 29-SEP-2000: 2000US-236891P.
 PR 02-OCT-2000: 2000US-237172P.
 PR 02-OCT-2000: 2000US-237173P.
 PR 02-OCT-2000: 2000US-237278P.
 PR 02-OCT-2000: 2000US-237294P.
 PR 02-OCT-2000: 2000US-237295P.
 PR 02-OCT-2000: 2000US-237316P.
 PR 03-OCT-2000: 2000US-237425P.
 PR 03-OCT-2000: 2000US-237588P.
 PR 03-OCT-2000: 2000US-237604P.
 PR 03-OCT-2000: 2000US-237606P.
 PR 03-OCT-2000: 2000US-237608P.
 PR 01-NOV-2000: 2000US-244867P.
 PR 01-NOV-2000: 2000US-245084P.
 XX (AVALON PHARM.
 PA Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 PI Sopet DR, Weaver Z;
 XX WPI: 2002-188264/24.
 DR
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1: SEQ ID 171; 44pp: English.

CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 3244 BP; 861 A; 795 C; 852 G; 736 T; 0 other:
 Query Match 62.6%; Score 2670.4; DB 24; Length 3244;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 3029; Conservative 0; Mismatches 1; Indels 348; Gaps 1;
 1 CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCAACCCCGGGCTGCTGCTTC
 DB 215 CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCAACCCCGGGCTGCTGCTTC 274
 QY 61 TCCATCCCGACCCGCGGGGGGCGGACCAACACAGTCCGGGAGAGCGTTGCCATTCC 120
 DB 275 TCCATCCCGACCCGCGGGGGGCGGACCAACACAGTCCGGGAGAGCGTTGCCATTTC 334
 QY 121 AAGTGACTGCAGCAGCAGCGGCGGCGCTCGGTTCTGAGCCCGACGCTGAAGGCA 180
 DB 335 AAGTGACTGCAGCAGCAGCGGCGGCGCTCGGTTCTGAGCCCGACGCTGAAGGCA 394
 QY 181 TTGCGCGTAGTCCATGCCCCGTAGAGAACTGTGCAGATGGATTAACTGCATGAGA 240
 DB 395 TTGCGCGTAGTCCATGCCCCGTAGAGAACTGTGCAGATGGATTAACTGCATGAGA 454
 QY 241 TATGGAAGAGACCGGGGATTGGTACCGTAACCATGTGTAGTGGGGTCTTCATCTGC 300
 DB 455 TATGGAAGAGACCGGGGATTGGTACCGTAACCATGTGTAGTGGGGTCTTCATCTGC 514
 QY 301 CTGCTGCTGTCACCATGTGCAACCTTGTCCGCGCGCCCTCTCTAGTTTAACTTGA 360
 DB 515 CTGCTGCTGTCACCATGTGCAACCTTGTCCGCGCGCCCTCTCTAGTTTAACTTGA 574
 QY 361 GATACCACATTAGAGCCAGAGGCCACCAACCAATATCAATCTCTACACAGAGTG 420
 DB 575 GATACCACATTAGAGCCAGAGGCCACCAACCAATATCAATCTCTACACAGAGTG 634
 QY 421 TACGTGCTGCGCCAGGGGAGTGCAGAGTGGCGGTCTTGAAAGATGCCGCGTG 480
 DB 635 TACGTGCTGCGCCAGGGGAGTGCAGAGTGGCGGTCTTGAAAGATGCCGCGTG 694
 QY 481 ATCAGTTGGACTAAGAGATGGGTGCACATTGGGGCCCAACATAGACAGTGTCTTATGGG 540
 DB 695 ATCAGTTGGACTAAGAGATGGGTGCACATTGGGGCCCAACATAGACAGTGTCTTATGGG 754
 QY 541 GAGTACTTCAGATTAAGGGCGCCACGCTTAGAGACTCGGCGCTTATCTGTACTGCC 600
 DB 755 GAGTACTTCAGATTAAGGGCGCCACGCTTAGAGACTCGGCGCTTATCTGTACTGCC 814
 QY 601 AGTAGACGTGTAGACGTGAACCTGTCTCATGTGGTATGTACAGATGCATCTCA 660
 DB 815 AGTAGACGTGTAGACGTGAACCTGTCTCATGTGGTATGTACAGATGCATCTCA 874
 QY 661 TCCGAGATGATGAGATGACACCGATGTCGGGAAGATTTTCTCAGTAGAAGAACTAAC 720
 DB 875 TCCGAGATGATGAGATGACACCGATGTCGGGAAGATTTTCTCAGTAGAAGAACTAAC 934
 QY 721 AACAGAGAGCACTACTGTGACCAACACAGAAAGATGAAAGCGGCTCCATGCTGTG 780
 DB 935 AACAGAGAGCACTACTGTGACCAACACAGAAAGATGAAAGCGGCTCCATGCTGTG 994
 QY 781 CCGTGGCCCAACCTGTCAAGTTTCCCTCCAGCGGGGGGAACCAATGGCAACCATG 840
 DB 995 CCGTGGCCCAACCTGTCAAGTTTCCCTCCAGCGGGGGGAACCAATGGCAACCATG 1054
 QY 841 CCGTGGCTAAAAACGGAAGGATTTAAGCAGAGCATGCAATTGGAGCTTACAAGGTA 900
 DB 1055 CCGTGGCTAAAAACGGAAGGATTTAAGCAGAGCATGCAATTGGAGCTTACAAGGTA 1114
 QY 901 CGAACCACCACTGAGCCTCATTTATGAAAGTGTGCCATCTGCACAAGGAAATTTAT 960
 DB 1115 CGAACCACCACTGAGCCTCATTTATGAAAGTGTGCCATCTGCACAAGGAAATTTAT 1174

```
OY 961 ACCTGTGTGAGAAATGAAATACGGGTCCATCATCATCAGCTACCACTGGATGTTGTG 1020
    |||
DB 1175 ACCTGTGTGTGAGATGAATACGGGTCCATCATCATCAGCTACCACTGGATGTTGTG 1234
OY 1021 GAGGATCGGCTCACCGGCCCATCTCTCAAGCCGAGCTGCCGGCAATGCTCTCACAGTG 1080
    |||
DB 1235 GAGGATCGGCTCACCGGCCCATCTCTCAAGCCGAGCTGCCGGCAATGCTCTCACAGTG 1294
OY 1081 GTGCGAGGAGACGTAGAGATTGTCTGCAAGGTTTACAGTATGCTCCAGCCCACTCCAG 1140
    |||
DB 1295 GTGCGAGGAGACGTAGAGATTGTCTGCAAGGTTTACAGTATGCTCCAGCCCACTCCAG 1354
OY 1141 TGCATCAAGCAGCTGGAAGAAAGAGAGTAATACGGGCCGAGCGGCTGCCCTACCTC 1200
    |||
DB 1355 TGCATCAAGCAGCTGGAAGAAAGAGAGTAATACGGGCCGAGCGGCTGCCCTACCTC 1414
OY 1201 AAGGTTCTCAAGGCGCGCGGTGTTAACACACGAGCAAGAGATTGAGGTTCTCTATATT 1260
    |||
DB 1415 AAGGTTCTCAAG----- 1426
OY 1261 CGGAATGTAACTTTTGAGACGCTGGGGAATATACGTGTTGGCGGTAATCTATTGGG 1320
    |||
DB 1427 ----- 1426
OY 1321 ATATCTTCTACTCTGCATGTTGACAGTTCTGCCAGCGCTGGAAAGAGAGATT 1380
    |||
DB 1427 ----- 1426
OY 1381 ACAGCTTCCAGACTACCTGAGATAGCATTTACTGCATAGGGTCTTCTTAATCGCC 1440
    |||
DB 1427 ----- 1426
OY 1441 TGTATGTTGTAACAGTATCTGTGCCAATGAGAACACAGCAAGAACAGCAGACTTC 1500
    |||
DB 1427 ----- 1426
OY 1501 AGCAGCCAGCGGCTGTGCACAAGCTGACCAAAAGTATCCCTCGCGAGACAGTTACA 1560
    |||
DB 1427 ----- 1426
OY 1561 GTTTCGGCTGAGTCCAGCTCTCATGAACCTCCAAACCCGCTGTGAGATTAACAACA 1620
    |||
DB 1427 GTTTCGGCTGAGTCCAGCTCTCATGAACCTCCAAACCCGCTGTGAGATTAACAACA 1486
OY 1621 CGCTCTCTTCAACGCGACAGACACCCCATGCTGGGAGGCTCCGAGTATGAACCTTCA 1680
    |||
DB 1487 CGCTCTCTTCAACGCGACAGACACCCCATGCTGGGAGGCTCCGAGTATGAACCTTCA 1546
OY 1681 GAGGACCCAAATGGGAGTTTCCAGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1740
    |||
DB 1547 GAGGACCCAAATGGGAGTTTCCAGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAA 1606
OY 1741 GGTTCGTTTGGGCAAGTGTCTATGGGGAAGCAGTGGGAATTGACAAAGACAGCCCAAG 1800
    |||
DB 1607 GGTTCGTTTGGGCAAGTGTCTATGGGGAAGCAGTGGGAATTGACAAAGACAGCCCAAG 1666
OY 1801 GAGGCGGTACCGTGGCGCTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTCT 1860
    |||
DB 1667 GAGGCGGTACCGTGGCGCTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTCT 1726
OY 1861 GATCTGTGTCTCAGAGATGAGATGAAGATGATTGGGAAACACAGAAATTCATTAAT 1920
    |||
DB 1727 GATCTGTGTCTCAGAGATGAGATGAAGATGATTGGGAAACACAGAAATTCATTAAT 1786
OY 1921 CTTTCTTGGAGCTGCACACAGAGATGGGCTCTATGTCTATGTTGAGTATGCTCTAAA 1980
    |||
DB 1787 CTTTCTTGGAGCTGCACACAGAGATGGGCTCTATGTCTATGTTGAGTATGCTCTAAA 1846
OY 1981 GGCACACCTCCGAGTACCTCGAGCCGAGCCGAGCCACCCGGGATGAGTACTCTATGAC 2040
    |||
DB 1847 GGCACACCTCCGAGTACCTCGAGCCGAGCCGAGCCACCCGGGATGAGTACTCTATGAC 1906

OY 2041 ATTAACCGTGTCTGAGAGCAGATGACCTTCAGAGACTTGTGTCTATGACACTACAG 2100
    |||
DB 1907 ATTAACCGTGTCTGAGAGCAGATGACCTTCAGAGACTTGTGTCTATGACACTACAG 1966
OY 2101 CTGGCCAGAGGACGTAGAGTACTTGGCTTCCCAAAAATGATTTCATGAGATTTAGACGC 2160
    |||
DB 1967 CTGGCCAGAGGACGTAGAGTACTTGGCTTCCCAAAAATGATTTCATGAGATTTAGACGC 2026
OY 2161 AGAAATGTTTGGTTAACACAGAAACAAATGTGATGAATAATAGCAGACTTGGACTCCGACA 2220
    |||
DB 2027 AGAAATGTTTGGTTAACACAGAAACAAATGTGATGAATAATAGCAGACTTGGACTCCGACA 2086
OY 2221 GATATCAACAATATAGACTATTCAAAAAGACCAACAAATGGGGGCTTCACATCAAGTGG 2280
    |||
DB 2087 GATATCAACAATATAGACTATTCAAAAAGACCAACAAATGGGGGCTTCACATCAAGTGG 2146
OY 2281 ATGGCTCCAGAAACCCCTGTTTGTATAGATATACATCATCAGAGTGTCTGTCTTC 2340
    |||
DB 2147 ATGGCTCCAGAAACCCCTGTTTGTATAGATATACATCATCAGAGTGTCTGTCTTC 2206
OY 2341 GGGGTGTTAATGTTGGGAGATCTTCACTTTAGGGGCTGCCCTACCCAGAGATTCCCTG 2400
    |||
DB 2207 GGGGTGTTAATGTTGGGAGATCTTCACTTTAGGGGCTGCCCTACCCAGAGATTCCCTG 2266
OY 2401 GAGGAACCTTTTAAGCTGCTGAAGAGACACAGAAATGATTAAGCCAGCAACTGACAC 2460
    |||
DB 2267 GAGGAACCTTTTAAGCTGCTGAAGAGACACAGAAATGATTAAGCCAGCAACTGACAC 2326
OY 2461 AACGAACCTACATGATGATGATGAGGACCTGTTGGCATGACAGTCCCTCCAGAGAACAG 2520
    |||
DB 2327 AACGAACCTACATGATGATGATGAGGACCTGTTGGCATGACAGTCCCTCCAGAGAACAG 2386
OY 2521 TTCACAGCTGTTGTAAGAACTTGGATGGAATTCACCTCTCACAACCAATAGCAATAC 2580
    |||
DB 2387 TTCACAGCTGTTGTAAGAACTTGGATGGAATTCACCTCTCACAACCAATAGCAATAC 2446
OY 2581 TTGGACCTTAGCCCAACCTCTGACAGAGTATTCACCTAGTACCTGACACAGAAATGCT 2640
    |||
DB 2447 TTGGACCTTAGCCCAACCTCTGACAGAGTATTCACCTAGTACCTGACACAGAAATGCT 2506
OY 2641 TGTTCCTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2700
    |||
DB 2507 TGTTCCTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2566
OY 2701 CCTCAGTATCCACATATAACGCGAGTGTAAACATGATGATGCTGTCCGCTGCC 2760
    |||
DB 2567 CCTCAGTATCCACATATAACGCGAGTGTAAACATGATGATGCTGTCCGCTGCC 2626
OY 2761 CAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGAGACCAATGCCCTCCAGAC 2820
    |||
DB 2627 CAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGAGACCAATGCCCTCCAGAC 2686
OY 2821 TGTTCCTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2880
    |||
DB 2687 TGTTCCTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTACGAACCATGCTT 2746
OY 2881 TATGTGTAAAGATTTATACAGTTGAAAACCTGTATCTTCCAGAGAGAGAAAGGTT 2940
    |||
DB 2747 TATGTGTAAAGATTTATACAGTTGAAAACCTGTATCTTCCAGAGAGAGAAAGGTT 2806
OY 2941 TCTGAGCAGCTGAGCTGCCACAGCCACCAATGTAAACCCCTGACACTGCCGTCTTG 3000
    |||
DB 2807 TCTGAGCAGCTGAGCTGCCACAGCCACCAATGTAAACCCCTGACACTGCCGTCTTG 2866
OY 3001 GCTGTGAGCAGCTAGAGCTCAAGGTGAGCGGCTTCCGCTCCCTGTATATTTTGTAA 3060
    |||
DB 2867 GCTGTGAGCAGCTAGAGCTCAAGGTGAGCGGCTTCCGCTCCCTGTATATTTTGTAA 2926
OY 3061 TAATTGAGAGATTTATGTCAGACACACTTACAGACACAAATGAGTATAGTGTC 3120
    |||
DB 2927 TAATTGAGAGATTTATGTCAGACACACTTACAGACACAAATGAGTATAGTGTC 2986
OY 3121 TGGATGTATGTAATAATATATTCAAATTAATGTATTAATATATTTACAGAGACT 3180
```



```

|||||
Db 1021 ACCTGCTGGCGGGTAAATCTATTGGATATCTTTCACCTCTCATGTTGACAGTTCTG 1080
|||
Qy 1354 CCAGCCCTGGAGAGAGAGAGATTAACTCCCGACAGACTACCTGGAGATAGCCATT 1413
|||
Db 1081 CCAGCCCTGGAGAGAGAGAGATTAACTCCCGACAGACTACCTGGAGATAGCCATT 1140
|||
Qy 1414 TACTGCATAGGGGCTCTTAAATCGCCTGTATGGTGTAAACATGCTGTCGCAATG 1473
|||
Db 1141 TACTGCATAGGGGCTCTTAAATCGCCTGTATGGTGTAAACATGCTGTCGCAATG 1200
|||
Qy 1474 AAGAAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
|||
Db 1201 AAGAAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
|||
Qy 1534 CGTATCCCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1593
|||
Db 1261 CGTATCCCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
|||
Qy 1594 AACACCCCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653
|||
Db 1321 AACACCCCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
|||
Qy 1654 GCAGGGGCTCCGAGATATACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1713
|||
Db 1381 GCAGGGGCTCCGAGATATACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
|||
Qy 1714 CTGACACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1773
|||
Db 1441 CTGACACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
|||
Qy 1774 GTGGGATTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1833
|||
Db 1501 GTGGGATTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
|||
Qy 1834 GATGATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1893
|||
Db 1561 GATGATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
|||
Qy 1894 ATTGGGAAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1953
|||
Db 1621 ATTGGGAAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
|||
Qy 1954 TATGTCATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2013
|||
Db 1681 TATGTCATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1740
|||
Qy 2014 CCACCCGGGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2073
|||
Db 1741 CCACCCGGGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1800
|||
Qy 2074 AAGGACTTGGTGTATGACACTTACAGTATGAGTATGAGTATGAGTATGAGTATGAG 2133
|||
Db 1801 AAGGACTTGGTGTATGACACTTACAGTATGAGTATGAGTATGAGTATGAGTATGAG 1860
|||
Qy 2134 AAATGATATTCATCGAGATTTAGACAGCAAAATGTTTGTAAACAGAAACATGTGATG 2193
|||
Db 1861 AAATGATATTCATCGAGATTTAGACAGCAAAATGTTTGTAAACAGAAACATGTGATG 1920
|||
Qy 2194 AAAATAGAGAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2253
|||
Db 1921 AAAATAGAGAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1980
|||
Qy 2254 ACCAATGGGGGCTTCCAGTCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2313
|||
Db 1981 ACCAATGGGGGCTTCCAGTCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2040
|||
Qy 2314 ACTATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2373
|||
Db 2041 ACTATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
|||
Qy 2374 GGCTGCCCTACCCAGAGAGATTCGGTGAAGAACTTTTAAAGCTGCTGAAGAGAGAGAC 2433
|||

```

```

Db 2101 GGCTGCCCTACCCAGAGAGATTCGGTGAAGAACTTTTAACTGCTGAAGAGAGAC 2160
|||
Qy 2434 AGAATGATTAAGCCAGCCAACTGACCAACGAAGTGTATGATGAGAGAGAGAGAGAG 2493
|||
Db 2161 AGAATGATTAAGCCAGCCAACTGACCAACGAAGTGTATGATGAGAGAGAGAGAGAG 2220
|||
Qy 2494 CATGAGTCCCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2553
|||
Db 2221 CATGAGTCCCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
|||
Qy 2554 CTCACCTCAGCAAGCAATGAGAGATTTGAGACCTCAGCAAGTGTATGATGAGAGAGAG 2613
|||
Db 2281 CTCACCTCAGCAAGCAATGAGAGATTTGAGACCTCAGCAAGTGTATGATGAGAGAGAG 2340
|||
Qy 2614 CCTAGTACCCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2673
|||
Db 2341 CCTAGTACCCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
|||
Qy 2674 GACCCGATGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2733
|||
Db 2401 GACCCGATGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
|||
Qy 2734 ACATGA 2739
|||
Db 2461 ACATGA 2466
|||

```

```

RESULT 7
AA014850
ID AA014850 standard; DNA; 2676 BP.
XX
XX AA014850;
AC
XX
XX
DT 18-FEB-1992 (first entry)
XX
DE Clone pTB1284 encoding complete FGF receptor.
XX
XX Human; fibroblast growth factor; cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 25..2334
FT CDS /*tag= a
FT
XX
XX W09117183-A.
XX
XX 14-NOV-1991.
PD
XX
XX 25-APR-1991; 91MO-JP00557.
PF
XX
XX 28-DEC-1990; 90JP-0415801.
PR 27-APR-1990; 90JP-0113146.
PR 31-JUL-1990; 90JP-0204438.
PR 14-SEP-1990; 90JP-0245256.
XX
XX
XX (TAKE ) TAKEDA CHEMICAL IND KK.
XX
XX Igarashi K, Senoo M, Watanabe T;
PI WPI; 1991-353723/48.
XX
XX P-PSDB; AAR15268.
DR
XX
XX New mutlein(s) of proteins - with fibroblast growth factor
PT receptor activity, useful for treating multiple endocrine
PT neoplasia, prostatic hypertrophy, used for diagnosis
XX
XX
XX Example 3; Fig 7; 88pp; English.
XX
XX A cDNA library prepared from human cancer cell line Kato III mRNA
CC was screened with an oligonucleotide corresponding to amino acids
CC 529-541 of chicken basic FGF receptor. Three positive clones were
CC obtained. One was cloned into pUC18/119 to give pTB1229 (see

```

CC AA014849). The complete FGF coding sequence was obtained by ligating
CC the insert from pT81229 to the DNA sequence of the plasmid pT81281
CC insert which encodes the carboxyl terminus of the FGF receptor from
CC Glu 533 onwards.

XX Sequence 2676 BP: 743 A; 645 C; 738 G; 550 T; 0 other;

Query Match 51.3%; Score 2188; DB 12; Length 2676;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 60; Indels 15; Gaps 2;

Oy 250 GGACGGGGGATGTGATACGTAACATGCTGAGCTGGGTGCTTTCATCTGCTGGTGTG 309
Db 1 GGACGGGGATGTGATACGTAACATGCTGAGCTGGGTGCTTTCATCTGCTGGTGTG 60
Oy 310 GTACCATGCAACCTTGTCCCTGGCCGGCCCTCTTCACTTATGTTAGAGATACACACA 369
Db 61 GTACCATGCGCAACCTTGTCCCTGGCCGGCCCTCTTCACTTATGTTAGAGATACACACA 120
Oy 370 TTAGAGCCAGAGAGACGACCAACCAATCTCTCAACCAAGAGTACGTGGCT 429
Db 121 TTAGAGCCAGAGAGACGACCAACCAATCTCTCAACCAAGAGTACGTGGCT 180
Oy 430 GCGCCAGGAGTGTGCTGAGAGTGGCTGCTGCTGTTGAAAGATGCCCGTGTAGTTGG 489
Db 181 GCGCCAGGAGTGTGCTGAGAGTGGCTGCTGCTGTTGAAAGATGCCCGTGTAGTTGG 240
Oy 490 ACTAAGATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
Db 241 ACTAAGATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Oy 550 CAGATTAAGGGGGGCGGCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
Db 301 CAGATTAAGGGGGGCGGCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 610 GTAGACAGTGAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
Db 361 GTAGACAGTGAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Oy 670 GATGAGATGACACCGATGCTGGGGAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 729
Db 421 GATGAGATGACACCGATGCTGGGGAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Oy 730 GACCATGCTGACCAACAGAAAGATGGAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 789
Db 481 GACCATGCTGACCAACAGAAAGATGGAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 540
Oy 790 AACACTGTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849
Db 541 AACACTGTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Oy 850 AAAAAGCGGAAGAGTTTAAAGAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909
Db 601 AAAAAGCGGAAGAGTTTAAAGAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Oy 910 CACTGAGCCTCTTATGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
Db 661 CACTGAGCCTCTTATGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Oy 970 GTGAGAAATGAATACGGGTGCTCATCATCAGCTACACCTGATGTTGTGAGCGATCG 1029
Db 721 GTGAGAAATGAATACGGGTGCTCATCATCAGCTACACCTGATGTTGTGAGCGATCG 780
Oy 1030 CCTACACGGGCGCTCTCTCAAGCGGAGCTGCGGGCAATGCTGCTGCTGCTGCTGCTG 1089
Db 781 CCTACACGGGCGCTCTCTCAAGCGGAGCTGCGGGCAATGCTGCTGCTGCTGCTGCTG 840
Oy 1090 GAGTGAAGTTTGTGCAAGGTTTACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
Db 841 GAGTGAAGTTTGTGCAAGGTTTACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Oy 1150 CACGTGAAAGAAAGCGAGTAATATACGGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTG 1209
Db 1150 CACGTGAAAGAAAGCGAGTAATATACGGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTG

Db 901 CACGTGAAAGAAAGCGAGTAATATACGGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTG 960
Oy 1210 AAGCGCGCGGCTGTTAACACACGACAGAAAGATGAGTTCTCTATTCGGAATGTA 1269
Db 961 AAGCACTCGGGATTAATATGTTCCCAATGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1014
Oy 1270 ACTTTTGGAGAGCGCTGGGGAATATACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1329
Db 1015 ACCGAGCGGATGCGGGGGAATATATATGTAAGTCTTCGCAATTTATATAGGCGACGCGCAAC 1074
Oy 1330 CACTGTGATGTTGACAGTTCTGCC-----ACGCGCTGGAAGAGAAAGAGATT 1380
Db 1075 CAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
Oy 1381 ACAGCTTCCCGACAGTACCTTGAGATAGCCATTATGCTGATAGAGGCTGCTGCTGCTGCTG 1440
Db 1135 ACAGCTTCCCGACAGTACCTTGAGATAGCCATTATGCTGATAGAGGCTGCTGCTGCTGCTG 1194
Oy 1441 TGTATGTTGTTAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1195 TGTATGTTGTTAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
Oy 1501 AGCAGCAGCGGCTGTGCTACAGCTGACCAAGCTATCCCTGCTGCGAGACAGCTAACA 1560
Db 1285 AGCAGCAGCGGCTGTGCTACAGCTGACCAAGCTATCCCTGCTGCGAGACAGCTAACA 1314
Oy 1561 GTTTCGCTGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1315 GTTTCGCTGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
Oy 1621 CGCCTCTCTTACCGGACAGACACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1375 CGCCTCTCTTACCGGACAGACACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
Oy 1681 GAGACCCCAAAATGGAGTTTCCAAAGATATAGCTGACACTGCTGCTGCTGCTGCTGCTG 1740
Db 1435 GAGACCCCAAAATGGAGTTTCCAAAGATATAGCTGACACTGCTGCTGCTGCTGCTGCTG 1494
Oy 1741 GGTGCTTGGGCAAGTGTGCTATGCGGAGCAGTGGGAATTTGCAAGAACAGCCCAAG 1800
Db 1495 GGTGCTTGGGCAAGTGTGCTATGCGGAGCAGTGGGAATTTGCAAGAACAGCCCAAG 1554
Oy 1801 GAGCGGTACACCGTGGCGGTGAAGTGTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 1555 GAGCGGTACACCGTGGCGGTGAAGTGTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1614
Oy 1861 GATCTGTGTGACAGATGAGATGATGAAATGATGTTGGGAAACCAAAATATCTTAAT 1920
Db 1615 GATCTGTGTGACAGATGAGATGATGAAATGATGTTGGGAAACCAAAATATCTTAAT 1674
Oy 1921 CTTCTTGGAGCTGTGACAGAGATGGGCTCTCTATGCTATGATGATGCTGCTGCTGCTG 1980
Db 1675 CTTCTTGGAGCTGTGACAGAGATGGGCTCTCTATGCTATGATGATGCTGCTGCTGCTG 1734
Oy 1981 GGCACCTTCGGAATTACCTCGAGCCGAGAGCCACCCGGGATGAGTACTCTATGAC 2040
Db 1735 GGCACCTTCGGAATTACCTCGAGCCGAGAGCCACCCGGGATGAGTACTCTATGAC 1794
Oy 2041 ATTTAACCGTGTCTGAGAGCAGATGACCTTCAAGAGCTTGTGTCATGACGATTTACACCC 2100
Db 1795 ATTTAACCGTGTCTGAGAGCAGATGACCTTCAAGAGCTTGTGTCATGACGATTTACACCC 1854
Oy 2101 CTGGCCAGAGGATGAGTACTTGGCTTCCCAAAATGATTTATCATCGAGATTTACACCC 2160
Db 1855 CTGGCCAGAGGATGAGTACTTGGCTTCCCAAAATGATTTATCATCGAGATTTACACCC 1914
Oy 2161 AGAAATGTTTGTAAACAGAAACCAATGTGTAATATGACAGCTTTGAGTGGCTGCCAGA 2220
Db 1915 AGAAATGTTTGTAAACAGAAACCAATGTGTAATATGACAGCTTTGAGTGGCTGCCAGA 1974
Oy 2221 GATATCAACAATATAGCTATTTACAAAAAGACCAACATGCGGCGCTTCCAGTCAAGTG 2280
Db 1975 GATATCAACAATATAGCTATTTACAAAAAGACCAACATGCGGCGCTTCCAGTCAAGTG 2034

QY 2281 ATGGCTCAGAACCCCTGTTGATAGATATACATCATGAGATGTCTGTCTTC 2340
 |||
 Db 2035 ATGGCTCAGAACCCCTGTTGATAGATATACATCATGAGATGTCTGTCTTC 2094
 |||
 QY 2341 GGGGTGTTAATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGGATTCGGTG 2400
 |||
 Db 2095 GGGGTGTTAATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGGATTCGGTG 2154
 |||
 QY 2401 GAGCACTTTTAAAGCTGCTGAAGAAAGACAGAAATGATTAAGCCAGCACTGCACC 2460
 |||
 Db 2155 GAGCACTTTTAAAGCTGCTGAAGAAAGACAGAAATGATTAAGCCAGCACTGCACC 2214
 |||
 QY 2461 AACCACTGATCATGATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAGAGCAAG 2520
 |||
 Db 2215 AACCACTGATCATGATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAGAGCAAG 2274
 |||
 QY 2521 TTCAACAGTTGGTAGAAGACTTGGATCGAATTTCTCACTCTCACAACCAATGAG 2574
 |||
 Db 2275 TTCAACAGTTGGTAGAAGACTTGGATCGAATTTCTCACTCTCACAACCAATGAG 2328
 |||
 RESULT 8
 AA014849
 ID AA014849 standard; DNA; 1954 BP.
 AC AA014849:
 XX
 DT 18-FEB-1992 (first entry)
 XX
 DE Clone pTB129 encoding protein with FGF receptor activity.
 XX
 KW Human; fibroblast growth factor; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 25..1953
 FT /tag= a
 PN WO9117183-A.
 PD 14-NOV-1991.
 PF 25-APR-1991; 91WO-JP00557.
 PR 28-DEC-1990; 90JP-0415801.
 PR 27-APR-1990; 90JP-0113146.
 PR 31-JUL-1990; 90JP-0204438.
 PR 14-SEP-1990; 90JP-0245256.
 PA (TAKE) TAKEDA CHEMICAL IND KK.
 PI Igarashi K, Senoo M, Watanabe T;
 DR WPL: 1991-353723/48.
 DR P-PSDB: AAR15267.
 PT New nuclein(s) of proteins - with fibroblast growth factor
 PT receptor activity, useful for treating multiple endocrine
 PT neoplasia, prostatic hypertrophy, used for diagnosis
 XX
 PS Example 2; Fig 4; 88pp; English.
 CC A cDNA library prepared from human cancer cell line Kato III mRNA
 CC was screened with an oligonucleotide corresponding to amino acids
 CC 529-541 of chicken basic FGF receptor. Three positive clones were
 CC obtained. One was cloned into pUC118/119 to give pTB128. The
 CC sequence of pTB129 was the longest of the three clones. See AA014848
 CC for pTB128 which lacks nucleotides 134-478 and 1309-1314 of
 CC pTB129 and has an A residue in stead of a T at the position
 CC corresponding to nucleotide 1029 of pTB129.
 CC

SQ Sequence 1954 BP; 531 A; 481 C; 544 G; 398 T; 0 other:
 Query Match 42.6%; Score 1817.2; DB 12; Length 1954;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 1887; Conservative 0; Mismatches 58; Indels 15; Gaps 2;
 QY 250 GGACCGGGATTTGGTACCCGTAACCATGTGACGTGGGGTCTTCATCTGCGCTG 309
 |||
 Db 1 GGACCGGGATTTGGTACCCGTAACCATGTGACGTGGGGTCTTCATCTGCGCTG 60
 |||
 QY 310 GTCACCATGGCAACTTGTCTCCCTGGCCCGCCCTCTCACTTAAATGAGATACACA 369
 |||
 Db 61 GTCACCATGGCAACTTGTCTCCCTGGCCCGCCCTCTCACTTAAATGAGATACACA 120
 |||
 QY 370 TTGAGCCAGAAAGCCACCACCAATATCTTCACAGAGTGAAGTGGCT 429
 |||
 Db 121 TTGAGCCAGAAAGCCACCACCAATATCTTCACAGAGTGAAGTGGCT 180
 |||
 QY 430 GCGCCAGGGGAGTGGTAGAGGTGGCGCTGTTGAAGATGCGCCGCTGATGAGTGG 489
 |||
 Db 181 GCGCCAGGGGAGTGGTAGAGGTGGCGCTGTTGAAGATGCGCCGCTGATGAGTGG 240
 |||
 QY 490 ACTAAGGATGGGGTGCACCTTGGGGCCCAACATAGACAGTGTCTTATTTGGAGTACTTG 549
 |||
 Db 241 ACTAAGGATGGGGTGCACCTTGGGGCCCAACATAGACAGTGTCTTATTTGGAGTACTTG 300
 |||
 QY 550 CAGATTAAGGGGCGCCACCGCTAGAGACTCGGCTCTATGCTTTGATGCGCAGTAGACT 609
 |||
 Db 301 CAGATTAAGGGGCGCCACCGCTAGAGACTCGGCTCTATGCTTTGATGCGCAGTAGACT 360
 |||
 QY 610 GTAGACAGTGAACCTTGTAATCTCATGATGATGTACAGATGCTCATGCTATGCGGAGAT 669
 |||
 Db 361 GTAGACAGTGAACCTTGTAATCTCATGATGATGTACAGATGCTCATGCTATGCGGAGAT 420
 |||
 QY 670 GATGAGATGACACCGATGGTGGGAAGATTTTGTCACTGAGAAGTAAACAACAAGAGA 729
 |||
 Db 421 GATGAGATGACACCGATGGTGGGAAGATTTTGTCACTGAGAAGTAAACAACAAGAGA 480
 |||
 QY 730 GCACCATCTGAGCCAAACAGAAAGATGGAAGACGGCTCATGCTGTGCTGGCGCC 789
 |||
 Db 481 GCACCATCTGAGCCAAACAGAAAGATGGAAGACGGCTCATGCTGTGCTGGCGCC 540
 |||
 QY 790 AACACTGTCAAGTTTGTGCTGCCAGCCGGGGGAACCAATGCAACCAATGCGGGTGG 849
 |||
 Db 541 AACACTGTCAAGTTTGTGCTGCCAGCCGGGGGAACCAATGCAACCAATGCGGGTGG 600
 |||
 QY 850 AAAAACGGGAAGAGTTTAAAGCAGAGATCGCATTTGAGGCTACAAAGGTAGCAAAACAG 909
 |||
 Db 601 AAAAACGGGAAGAGTTTAAAGCAGAGATCGCATTTGAGGCTACAAAGGTAGCAAAACAG 660
 |||
 QY 910 CACTGAGGCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAATTAATCTGTGTG 969
 |||
 Db 661 CACTGAGGCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAATTAATCTGTGTG 720
 |||
 QY 970 GTGAGAAATGAATACGGGTGCATCAATCAACAGTACACCTGGATGTTGGAGGATGG 1029
 |||
 Db 721 GTGAGAAATGAATACGGGTGCATCAATCAACAGTACACCTGGATGTTGGAGGATGG 780
 |||
 QY 1030 CCTCACCGGCCCATCTCTCAAGCCGGAGTCCGGCAAAATGCTTCCACAGTGTGGAGGA 1089
 |||
 Db 781 CCTCACCGGCCCATCTCTCAAGCCGGAGTCCGGCAAAATGCTTCCACAGTGTGGAGGA 840
 |||
 QY 1090 GAGGTAGAGTTGTCTGCAAGTTTATCAATGATGCCACCCCAACATTCAGTGGATCAAG 1149
 |||
 Db 841 GAGGTAGAGTTGTCTGCAAGTTTATCAATGATGCCACCCCAACATTCAGTGGATCAAG 900
 |||
 QY 1150 CACGTGGAAAGAACGGCAGTAATACGGGCCGAGCGGCTCCCTACCTCAAGGTTCTC 1209
 |||
 Db 901 CACGTGGAAAGAACGGCAGTAATACGGGCCGAGCGGCTCCCTACCTCAAGGTTCTC 960
 |||
 QY 1210 AAGCGCCCGGGTGTAAACCAACGGAAGATTTAGAGTCTCTAATATTCGAATGTA 1269
 |||
 Db 961 AAGCACTCGGGATTAATAGTTCAATGCAGAAAGTGTGCTGTCTC-----AATGTG 1014
 |||

Qy	1270	ACGTTTAGAGACGCTGGGAAATATACGTCCTTGGGGGTAATTCATATGGGATATCCCTTT	1323
Db	1015	ACCAGGCGGATCGGGGGAAATATATATTAAGGTCCTCAATATATATATGGGCGAGCCAAAC	1074
Qy	1330	CACGCTCATAGTTGACAGAGTTGTGCC-----AGCGCCGTGAAGAGAAAGAGATT	1380
Db	1075	CAGCTCTCGCTGCTCACTGTCTCTGCCAAACAGCAACGCCCTGGGAAGAAAGAGATT	1134
Qy	1381	ACAGCTTCCCAAGTACTACGTGAGATAGCCATTATCTGCATAGGGGCTTCTTAATGCC	1440
Db	1135	ACACGCTTCCCAAGCTACGTGAGATAGCCATTATCTGCATAGGGGCTTCTTAATGCC	1194
Qy	1441	TGTTATGCTGTAACAGTCACTCTGTCCGAATGAAGAACACAGCCAAACCGACGATTC	1500
Db	1195	TGTTATGCTGTAACAGTCACTCTGTCCGAATGAAGAACACAGCCAAACCGACGATTC	1254
Qy	1501	AGCAGCAGCGGCGTGTGCACAGCTGACCAACGATCCCGTCCGAGACAGGTAA	1560
Db	1255	AGCAGCAGCGGCGTGTGCACAGCTGACCAACGATCCCGCTCCGAGACAGGTAA	1314
Qy	1551	GTTTGGGCTAGTCCAGCTCTCCATGAACCTCAACACCCCGCTGGTAGATAACA	1620
Db	1315	GTTTGGGCTAGTCCAGCTCTCCATGAACCTCAACACCCCGCTGGTAGATAACA	1374
Qy	1621	CGCCTCTCTTCAAGGCGACACCCTCATGTCTGCGACGGGTTCCGAGATGAACCTTCA	1680
Db	1375	CGCCTCTCTTCAAGGCGACACCCTCATGTCTGCGACGGGTTCCGAGATGAACCTTCA	1434
Qy	1681	GAGAACCCAAATACGAGTTTCCAAAGATTAAGCTACACTGGGCAAGCCCTGGAGAA	1740
Db	1435	GAGAACCCAAATATGGAGTTTCCAAAGATTAAGCTACACTGGGCAAGCCCTGGAGAA	1494
Qy	1741	GGTTGCTTTGGGCAAGTGTCTATGGCGGAAGCAGTGGGATTTGACAAAGACAGCCCAAG	1800
Db	1495	GGTTGCTTTGGGCAAGTGTCTATGGCGGAAGCAGTGGGATTTGACAAAGACAGCCCAAG	1554
Qy	1801	GAGCGGCTCACGCTGGCCCTGGAAGATGTTGGAAAGATGATGCCACAGAAAGACCTTCT	1860
Db	1555	GAGCGGCTCACGCTGGCCCTGGAAGATGTTGGAAAGATGATGCCACAGAAAGACCTTCT	1614
Qy	1851	GATCTGGTGTACAGATGAGATGATGAAGATGATGGGAACACAAAGATATCTAAAT	1920
Db	1615	GATCTGGTGTACAGATGAGATGATGAAGATGATGGGAACACAAAGATATCTAAAT	1674
Qy	1921	CTTCTTGGAGCTTGACACAGATGGGCGCTCTCTATGTATGATTGAGTAGTCCCTTAA	1980
Db	1675	CTTCTTGGAGCTTGACACAGATGGGCGCTCTCTATGTATGATTGAGTAGTCCCTTAA	1734
Qy	1981	GGCAACCTCCGAAGATACCTCCGACCCCGGAGGCCACCCGGGATGAGATCTCTATGAC	2040
Db	1735	GGCAACCTCCGAAGATACCTCCGACCCCGGAGGCCACCCGGGATGAGATCTCTATGAC	1794
Qy	2041	ATTAAACGTTTCTGTGAGAGACGATGACCTTCAAGAGCTTGGTGTCAATGCACCTACAG	2100
Db	1795	ATTAAACGTTTCTGTGAGAGACGATGACCTTCAAGAGCTTGGTGTCAATGCACCTACAG	1854
Qy	2101	CTGGCCAGAGCATGAGTACTTGGCTTCCCAAAAATGATTATTCATCGAGATTTAGCACC	2160
Db	1855	CTGGCCAGAGCATGAGTACTTGGCTTCCCAAAAATGATTATTCATCGAGATTTAGCACC	1914
Qy	2161	AGAAATGTTTGGTAAACAGAAACAAATGTGTATGAATAATAG 2200	
Db	1915	AGAAATGTTTGGTAAACAGAAACAAATGTGTATGAATAATAG 1954	

RESULT 9
AAQ14851
ID AAQ14851 standard; DNA; 2310 BP.

XX	DE	Clone pTB1283 encoding complete FGF receptor.
XX	XX	
XX	KW	Human; fibroblast growth factor; cancer; ss.
XX	XX	
XX	OS	Homo sapiens.
XX	XX	
XX	FT	Key
XX	FT	25.1983
XX	FT	CDS
XX	XX	Location/Qualifiers
XX	XX	/*tag= a
XX	PN	W09117183-A.
XX	PD	
XX	XX	14-NOV-1991.
XX	XX	
XX	PE	25-APR-1991: 91WO-JP00557.
XX	XX	
XX	PR	28-DEC-1990: 90JP-0415801.
XX	PR	27-APR-1990: 90JP-0113146.
XX	PR	31-JUL-1990: 90JP-0204438.
XX	PR	14-SEP-1990: 90JP-0245256.
XX	PA	(TAKE) TAKEDA CHEMICAL IND KK.
XX	XX	
XX	PI	Igarashi K, Senoo M, Watanabe T;
XX	XX	
XX	DR	WPI: 1991-353723/48.
XX	DR	P-PSDB: AAR15269.
XX	XX	
XX	PT	New mutin(s) of proteins - with fibroblast growth factor
XX	PT	receptor activity, useful for treating multiple endocrine
XX	PT	neoplasia, prostatic hypertrophy, used for diagnosis
XX	XX	
XX	XX	Example 3: Fig 8; 88pp; English.
XX	XX	
XX	CC	A cDNA library prepared from human cancer cell line Kato III mRNA
XX	CC	was screened with an oligonucleotide corresponding to amino acids
XX	CC	529-541 of chicken basic FGF receptor. Three positive clones were
XX	CC	obtained. One was cloned into pUC118/119 to give pTB128 (see
XX	CC	AA014848). The complete FGF coding sequence was obtained by ligating
XX	CC	the insert from pTB128 to the DNA sequence of the plasmid pTB1281
XX	CC	insert which encodes the carboxyl terminus of the FGF receptor from
XX	CC	Glu 533 onwards.
XX	XX	
XX	XX	Sequence 2310 BP; 629 A; 566 C; 636 G; 479 T; 0 other;

QY	1088	GAGACGTAGAGTTTGTCTGCAAGCTTTACAGTATGTCACAGCCCCACATCCAGTGGATCA	1147
Db	494	GAGAGCTGAGATTGTGTCTGCAAGGTTTACAGTATGCCAGCCCCACATCCAGTGGATCA	553
QY	1148	AACACGTGTAAAAAGAACGGCAGTAAATAGCGGGCCGACGGGGCGCTCCCTACCTCAAGTTC	1207
Db	554	AGCACGTGTAAAAAGAACGGCAGTAAATAGCGGGCCGACGGGGCGCTCCCTACCTCAAGTTC	613
QY	1208	TCAGGCCGCGGTGTTAACACCAAGACAGCAAGATGTAAGTTCTCTATATTCGGAATG	1267
Db	614	TCMAACACTCGGGGATAAATAGTTCCAAATCAGAAAGCGCTGGCTCTG-----TCAAATG	667
QY	1268	TAAACTTTTGAAGAGCGTGGGAAATATACGTCCTTGGCGGGTATTTCTATATGGGATATCTT	1327
Db	668	TCACCGAGGCGGATGTCTGGGAAATATATATGTAAGTTCTTCCAAATTTATATAGGCGAGGCA	727
QY	1328	TTCACTTCGCATGGTTAGACATTTCTGGC-----AGCGCTGGAGAGAAAAAGAGA	1378
Db	728	ACCAATGTCCCTGGCTCACTGTCTCTGCCAAMACAGCAAGCGCTGGAAGAAAAAGAGA	787
QY	1379	TTACAGCTTCCCGCACTACCTCGAGATACCAATTACTGCATAGGGGTCTTTCTTAATCG	1438
Db	788	TTACAGCTTCCCGCACTACCTCGAGATACCAATTACTGCATAGGGGTCTTTCTTAATCG	847
QY	1439	CCTGTATGTTGTTAAACAGTATCTCTGGCCGATGAAAGAACAGCAAGAACCCAGACT	1498
Db	848	CCTGTATGTTGTTAAACAGTATCTCTGTGCGGAATGAAGAACAGCAAGAACCCAGACT	907
QY	1499	TCAGACAGCCAGCCGGCTGTGCACACAGTGCACCAACGTAATCCCTCGCGAGACAGTTAA	1558
Db	908	TCAGACAGCCAGCCGGCTGTGCACACAGTGCACCAACGTAATCCCTCGCGAGAGACAG-----	963
QY	1559	CAGTTTGGGCTGATGCCAGCTCCCTCCATGAATCCCAACACCCCGGTGGTGAAGATAAACA	1618
Db	964	---GTTTGGGCTGATGCCAGCTCCCTCATGAATCCCAACACCCCGGTGGTGAAGATAAACA	1021
QY	1619	CACGCTCTCTTTCAAGGGCAGACACCCCATGCTGGCAGAGGGTCTCCGAGTATGAATTC	1678
Db	1022	CACGCTCTCTTTCAAGGGCAGACACCCCATGCTGGCAGAGGGTCTCCGAGTATGAATTC	1081
QY	1679	CAGAGSAGCCCAAAATGGSAGTTTTCAAAGAGATTAAGTGCACACTGGGGCAAGCCCTGGGAG	1738
Db	1082	CAGAGSAGCCCAAAATGGSAGTTTTCAAAGAGATTAAGTGCACACTGGGGCAAGCCCTGGGAG	1141
QY	1739	AAGTTGCTTTGGGCAAGTGTGATGGCGGAGACATGGGAATTTGACAAAGACAAGCCCA	1798
Db	1142	AAGTTGCTTTGGGCAAGTGTGATGGCGGAGACATGGGAATTTGACAAAGACAAGCCCA	1201
QY	1799	AGSAGGGGTTCACCGTGGCCGTCAAAATGTTGAAGATGATCCACAGAGAAAGACCTTT	1858
Db	1202	AGSAGGGGTTCACCGTGGCCGTCAAAATGTTGAAGATGATCCACAGAGAAAGACCTTT	1261
QY	1859	CTGATCTGTGTGTCAGAGATGAGATGATGAAGTGAATTTGGGAAACACAAGAAATTAATAA	1918
Db	1262	CTGATCTGTGTGTCAGAGATGAGATGATGAAGTGAATTTGGGAAACACAAGAAATTAATAA	1321
QY	1919	ATCTTTTGGAGCCTGCACACAGATGGGCTCTCTATGTCAATAGTTAGTATGATCCCTTA	1978
Db	1322	ATCTTTTGGAGCCTGCACACAGATGGGCTCTCTATGTCAATAGTTAGTATGATCCCTTA	1381
QY	1979	AAGCAACCTCCGGAATTAACCTCCGAGACCCGGAGGCACCCGGGATGGAGTACATCCATATG	2038
Db	1382	AAGCAACCTCCGGAATTAACCTCCGAGACCCGGAGGCACCCGGGATGGAGTACATCCATATG	1441
QY	2039	ACAATTAACCGTTCCTGAGAGACAGATGACCTTCAGAGACTTGGTGTGCATGACACTTACC	2098
Db	1442	ACAATTAACCGTTCCTGAGAGACAGATGACCTTCAGAGACTTGGTGTGCATGACACTTACC	1501
QY	2099	AGCTGGCCAGAGGATGAGATACTTGGTCTTCCCAAAATGTAATTCATGGAATTTTACAG	2158
Db	1502	AGCTGGCCAGAGGATGAGATACTTGGTCTTCCCAAAATGTAATTCATGGAATTTTACAG	1561

QY	2139	CCGAAATGTTTGGTGAACGAAAAACAAATGTGATGAAATAGACACTTTGGACTCGCA	2218
Db	1562	CCAGAAATGTTTGGTGAACGAAAAACAAATGTGATGAAATAGACACTTTGGACTCGCA	1621
QY	2219	GAGATATCAACAAATATGACATATTACAAAAAGACCAATGGGGGGCTTCCAGTCAGT	2278
Db	1622	GAGATATCAACAAATATGACATATTACAAAAAGACCAATGGGGGGCTTCCAGTCAGT	1681
QY	2279	GGATGGCTCCGAAAGCCCTGTTTGATAGATATACACTCATGAGTGTGCTGTGCT	2338
Db	1682	GGATGGCTCCGAAAGCCCTGTTTGATAGATATACACTCATGAGTGTGCTGTGCT	1741
QY	2339	TCGGGGGTATATGTGGGAATCTTCACTTTAGGGGGCTGCGCCATCCAGGAGATTCCG	2398
Db	1742	TCGGGGGTATATGTGGGAATCTTCACTTTAGGGGGCTGCGCCATCCAGGAGATTCCG	1801
QY	2399	TGAGAGAACTTTTAACTCTCTGAGGAAGGACACAGATGGATTAAAGCAGCAACTCA	2458
Db	1802	TGAGAGAACTTTTAACTCTCTGAGGAAGGACACAGATGGATTAAAGCAGCAACTCA	1861
QY	2459	CCAAAGAACTGTACATGATGATGAGGAGCTGTTGGCAGTCAGTGGCCCTCCAGAGACCA	2518
Db	1862	CCAAAGAACTGTACATGATGATGAGGAGCTGTTGGCAGTCAGTGGCCCTCCAGAGACCA	1921
QY	2519	CGTTTCAAGCAATGGTGAAGAGCTTGGATCGAATTCACCTCTCAACAACAAATGAG	2574
Db	1922	CGTTTCAAGCAATGGTGAAGAGCTTGGATCGAATTCACCTCTCAACAACAAATGAG	1977

```

RESULT 10
AAQ14049
ID      AAQ14049 standard; cDNA; 2345 BP.
XX
XX
AC      AAQ14049;
XX
XX      17-DEC-2001 (updated)
DT      09-JAN-1992 (first entry)
XX
XX      Human ect gene.
DE
XX      Keratinocyte growth factor receptor; KGF; tyrosine kinase; ss.
XX
XX      Homo sapiens.
XX
XX      Key
FH      CDS
FT      Location/Qualifiers
FT      130..2310
FT      /*tag= a
FT      250..2307
FT      /*tag= b
FT      187..249
FT      sig_peptide
FT      /*tag= c
XX
XX      USN7560035-N.
XX
XX      10-SEP-1991.
XX
XX      09-AUG-1990; 90US-0560035.
XX
XX      09-AUG-1990; 90US-0560035.
XX
XX      (USSH ) NAT INST OF HEALTH.
XX
XX
XX      Miki T, Aaronson SA, Fleming T;
XX
XX      WPT; 1991-310282/42.
XX
XX      P-PSDB; AAR14280.
XX
XX      New genetic cloning vectors - which provide efficient, automatic
XX      directional cloning of cDNA copy of a eukaryotic mRNA.
XX
XX      Disclosure; Fig 15; 108pp; English.
XX
XX      The sequence was obt'd. from a clone isolated from a cDNA library

```



```
OY 2639 CTGTCTTCTCAGAGATGATTCGTGTTTTCTCCAGACCCCATCCCTTAGAACCATGCC 2698
      |||||||
Db 2210 CTGTCTTCTCAGAGAGATTCGTGTTTTCTCCAGACCCCATCCCTTAGAACCATGCC 2269
OY 2699 TTCTCTGATTCACACATTAAGCGAGTGTAAATGATGACTGTGTCTGCTGTCC 2758
      |||||||
Db 2270 TGCTCTGATTCACACATTAAGCGAGTGTAAATGATGATGATGATGATGATGATG 2329
OY 2759 CCCAAGCAGACAGCA 2774
      |||||||
Db 2330 CCCAAGCAGACAGCA 2345

RESULT 11
AAO10868
ID AAO10868 standard; cDNA; 2345 BP.
XX
AC AAO10868;
XX
DT 09-MAY-1991 (first entry)
XX
DE KGF receptor gene.
XX
KM Keratinocyte growth factor; ect1; tyrosine kinase;ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 187..249
FT mat_peptide /tag= a
FT /tag= b
FT /label= KGF receptor
XX
PN WO9102077-A.
XX
PD 21-FEB-1991.
XX
PF 30-JUL-1990; 90MO-US04239.
XX
PR 28-JUL-1989; 89US-0386053.
XX
PA (USDC ) US SEC OF COMMERCE.
XX
PI Miki T, Aaronson SA, Fleming T;
XX
DR WPI: 1991-073549/10.
XX
P-PSDB; AAR10933.
XX
PT Efficient genetic cloning system - useful for cloning cDNA copies
PT of eukaryotic mRNAs of all sizes and for library preparation
XX
PS Disclosure; Fig 15a; 103bp; English.
XX
CC The ecl1 sequence encoding the KGF receptor was obt'd. from a clone
CC isolated from a BALB/MK epidermal keratinocyte DNA library prep'd.
CC using the lambda pCEV27 cloning system of the invention. The protein
CC appears to typical transmembrane tyrosine kinase (see AAR10933 for
CC details), closely related to the mouse bFGF receptor.
CC See also AAO10867.
XX
SQ Sequence 2345 BP; 621 A; 602 C; 634 G; 488 T; 0 other:

Query Match 38.5%; Score 1642.8; DB 12; Length 2345;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1814; Conservative 0; Mismatches 227; Indels 15; Gaps 2;
```

```
Db 356 CCAACACTGTGAAGTTCCCGCTGTCGGGCGGAATCCAAACCCACATAGTGTGT 415
OY 848 TGAATAACGGGAAGAGATTAAACAGAGCATGCATTGGAGGCTTACAGTACGAAC 907
      |||||||
Db 416 TAAATAACGGGAAGAGATTAAACAGAGCATGCATTGGAGGCTTAAAGTACGAAC 475
OY 908 AGCAGTGGAGCCCTTATTCGAAAGTGTGTCCCATCTGACAAAGGAATTAATACCTGTG 967
      |||||||
Db 476 AGCAGTGGAGCCCTTATTCGAAAGTGTGTCCCATCTGACAAAGGAATTAATACCTGTG 535
OY 968 TGGTGGAGATGAATAGAGGTGCTCCATACACAGTACACCTGATGTTGTGGAGCGAT 1027
      |||||||
Db 536 TGGTGGAGATGAATAGAGGTGCTCCATACACAGTACACCTGATGTTGTGGAGCGAT 595
OY 1028 CGGCTACCGGCGCCATCTCCAAAGCCGAGCTGCGGCAATAGCTTCACAGTGTGGAG 1087
      |||||||
Db 596 CACACACCGGCGCCATCTCCAAAGCTGAGCTGCTCAATAGCTTCACAGTGTGGAG 655
OY 1088 GAGAGTGAAGTTGTTGTCGAGAGTTTACAGTATGTCGCCACGCCCATTCAGTGAATCA 1147
      |||||||
Db 656 GGGATGTGAGTTTCTCTGAGAGTTTACAGAGATGCCACGCCCATTCAGTGAATCA 715
OY 1148 AGCAGCTGGAATAAGAACGGCAGTAAATACGGGCCGACGGGCTGCCCTACCTCAAGTTC 1207
      |||||||
Db 716 AGCAGCTGGAATAAGAACGGCAGTAAATACGGGCTGATGGCTGCTCCTACCTCAAGTTC 775
OY 1208 TCAAGCCCGCCGGTGTAAACCCACGAGCAAGAGATTGAGTTCTATATTCCGAGATG 1267
      |||||||
Db 776 TGAAGCAGTCCGGGATTAATAGCTCCAAATGCAAGATGCTGCTGCTGCTC-----AATG 829
OY 1268 TAACTTTTGAAGGAGCGCTGGGGAATATACGCTGTGGCGGATTAATCTATGGAGATATCT 1327
      |||||||
Db 830 TGAAGGAGATGATGATGCTGGGGAATATATATGTAAGTCTCCAAATATATATATATATAT 889
OY 1328 TTCACTCTCATGATGTTGACAGTCTTCC-----AGCGCTGGAAGAGAAAGAGAGA 1378
      |||||||
Db 890 ACCAGTCTGCTGGCTCACTGTCCTGCCAAACAGCAACGCCCTGTGAGAGAAAGAGAGA 949
OY 1379 TTACAGCTTCCCGACAGTACCTGAGATAGCCATTACTGCTAGAGGCTCTTCTTAATCG 1438
      |||||||
Db 950 TCACGGCTTCCCGACAGTATTCGAGATAGCTATTAATGCTAGAGGCTCTTCTTAATCG 1009
OY 1439 CCTGATGTGTGTAACAGTATCTCTGCGGAATGAAGAACGACGACCAAGCCAGACT 1498
      |||||||
Db 1010 CCTGATGTGTGTAACAGTATCTCTGCGGAATGAAGAACGACGACCAAGCCAGACT 1069
OY 1499 TCAGCAGCCAGCGGCTGTGACAAAGCTGACCAACAGTATCCCTGCGGAGACAGTAA 1558
      |||||||
Db 1070 TCAGCAGCCAGCGGCTGTGACAAAGCTGACCAACAGTATCCCTGCGGAGACAGTAA 1129
OY 1559 CAGTTTGGGCTGATGTCAGCTCTCTCATGAACTCCACACCCCGCTGAGATTAACAA 1618
      |||||||
Db 1130 CAGTTTGGGCTGATGTCAGCTCTCTCATGAACTCCACACCCCGCTGAGATTAACAA 1189
OY 1619 CAGGCTCTCTTCAACGCGACAGCCCATGCTGGAGGGGTCTCCAGATGAATCACTC 1678
      |||||||
Db 1190 CGGCTCTGCTCTCAACAGCGGACACCCGATGCTGACGGGGTCTCCAGATGAGTGGC 1249
OY 1679 CAGAGCAGCCAAATGGAATTTCCAAAGATTAACCTGAGCAAGCCCTGAGAG 1738
      |||||||
Db 1250 CAGAGGATTCAAAGTGGGAATTTCCCAAGATTAACCTGAGCAAGCCCTGAGAG 1309
OY 1739 AAGTTTGTGGGGAATGATGATGATGGGGAAGCAAGTGGGAATTAACAAAGCAAGCCCA 1798
      |||||||
Db 1310 AAGTTTGTGGGGAATGATGATGATGGGGAAGCAAGTGGGAATTAACAAAGCAAGCCCA 1369
OY 1799 AAGAGCGGCTGACCTGCGCGGTGAAGATGTTGAAGATGATGATGATGATGATGATGAT 1858
      |||||||
Db 1370 AAGAGCGGCTGACCTGCGCGGTGAAGATGTTGAAGATGATGATGATGATGATGATGAT 1429
OY 1859 CTGATCTGTGTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1918
      |||||||
Db 1430 CTGATCTGTGTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1489
```


DR WPI: 1999-418269/35.
DR P-PSDB: AAY23631.

XX Distinguishing between the biological activities of acidic and
PT non-acidic fibroblast growth factor proteins

XX Disclousure: Columns 27-32; 44pp; English.

XX The specification describes a method for differentiating biological
CC activities among the full length form of acidic fibroblast growth
CC factor (aBFGF) proteins and other non-acidic fibroblast growth factor
CC (non-aBFGF) proteins. FGF proteins are thought to be involved in wound
CC healing and tissue repair. The method comprises determining and comparing
CC the mitogenic responses of Tr31-5-1 (ATCC CRL-12521) and Tr33-1-2
CC (ATCC CRL12522) cell lines to different forms of aBFGF and non-aBFGF
CC proteins. The method may be used for differentiating biological
CC activities among the full length form and truncated forms of aBFGF
CC proteins and other (non-aBFGF) proteins. The information thus obtained
CC may be used to better understand the molecular basis of the multiple
CC functions of FGF activity in physiological and pathological conditions.
CC This understanding provides the basis for the rational design of both
CC ligand and FGF receptor agonists and antagonists. The present
CC sequence encodes bek-like newt fibroblast growth factor receptor FGFR2.

XX Sequence 2675 BP; 684 A; 716 C; 705 G; 570 T; 0 other:

Query Match 32.0%: Score 1367.6; DB 20; Length 2675;

Best Local Similarity 79.1%: Pred. No. 0;

Matches 1554; Conservative 0; Mismatches 429; Indels 9; Gaps 2;

Qy 648 AGATGCCATCTCATCCGAGATGATGAGTACACACCGATGTCGGGAAGATTGTCAG 707
Db 432 AGATGCCAATCATCATCGGATGATGATGAGTACACACGCGCTCGAAGATTTCACAA 491
Qy 708 TGGAGAACATACACAAAGAGAGACCATGAGACACAGAGAAATGGAAGAG 767
Db 492 TGGAGAAC--AAACCATAGAGGCTCCGTACGAGCAATGAGAAATTTGGAAGAA 548
Qy 768 GGTTCATGCTGTCGCTGCGGCAACACTGTCAAGTTTCGCTCCGACCGGGGGAAACC 827
Db 549 ACTCCATGCTGTCGCGCTGCGGCAACACTGTGAATTCGCTGTCGACCGGGGGCAACC 608
Qy 828 AATGCCAACCATGCGGTGCTGAAAAACGGGAAGAGTTTAAAGCAGACATGCGATTGG 887
Db 609 TACGCCCTCATGAGGTGCTGAGAAAGGCAAGAGATTCAAGCAGACACCGCATGG 668
Qy 888 AGGCTTCAAGTACGAAACAGCAGCTGAGGCTCATATGAGAAAGTGTGCTCCATCTGA 947
Db 669 CGGCTTCAAGTACGAGTACGAACTTCAAGCTGATCATGAGAGGCTGCTCCCTGTA 728
Qy 948 CAAGGAAATTTTACCTGTGTGTGAGAAATGATACGGGTCCATCATACACAGTACCA 1007
Db 729 CGAGGCAATCATACCTGTATCATGAGAAAGATGTGATCATCATATCACACCTACCA 788
Qy 1008 CCTGATGTTTGTGAGCGATTCGCTACCGGCCCATCTTCACACCGGACTCCCGCAAA 1067
Db 789 CCTGATGTTTGTGAGCGGCTACCGGCCCAATCTTCACACCGGCTTCCGCAAA 848
Qy 1068 TGGCTTCCAAAGTGTGCGAGAGAGCTAGATTTGTCTCAAGGTTTACAGTATGCCCA 1127
Db 849 CACAAACCAAAAGTGGGGGCGATGCAAGTTTGTTCGAAAGTCTTACAGTACGCCACA 908
Qy 1128 GCCCCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1187
Db 909 GCCACATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
Qy 1188 GCTGCCCTTACCTCAAGTTCTCAAGGCCCGCGTGTAAACACACGACGACAAAGATTA 1247
Db 969 GCATCCCTTATGAAAGTCTTAAAGCGCGCGTGTAAACACACGACGACAAAGATTA 1028
Qy 1248 GGTCTCTATTTATGGAATGATTTTATGAGAGCTGGGGAAATATAGTGTGCGGG 1307
Db 1029 ACTCTCTATTTATGGAATGATTTTATGAGAGCTGGGGAAATATAGTGTGCGGG 1088

Qy 1308 TAATTTATGGAATATCCCTTTCACTGTGATGATGATGATGATGATGATGATGATGAT 1367
Db 1089 TAATTTATGGAATATCCCTTTCACTGTGATGATGATGATGATGATGATGATGATGAT 1148
Qy 1368 AGAAAGAGATTTACAGCTTCCCAAGTACCTGAGATAGGCAATTTACTGATAGGCT 1427
Db 1149 GGAAGTGA-----TTCACTATCGAGATATACGAAATTCGCAATCTGATGAGGAG 1202
Qy 1428 CTTCTTAATGCGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1487
Db 1203 CTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
Qy 1488 GAAGCAGATTTACAGCTTCCCAAGTACCTGAGATAGGCAATTTACTGATAGGCT 1547
Db 1263 GAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322
Qy 1548 GAGACAGTATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1607
Db 1323 CAGACAGTATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1382
Qy 1608 GAGGATACAAACAGGCTTCTTCAAGCGAGACACCCCATGCTGGGAGGCTGCCGA 1667
Db 1383 CCGGATCACACTCCGCTGCTTCAACATGACACCCCATGCTGGGAGGCTGCCGA 1442
Qy 1668 GTATGAATTTCCAGAGAGACCCAAATGAGAGTTTCCAGAGATTAAGTACACTGGCA 1727
Db 1443 GTATGAAGTGTGAG 1502
Qy 1728 GCCCTGGGAGAGAGTGTGCTTGGGCAAGTGTGATGCGGAGAGAGAGAGAGAGAGAG 1787
Db 1503 GCCCTGGGAGAGAGTGTGCTTGGGCAAGTGTGATGCGGAGAGAGAGAGAGAGAGAG 1562
Qy 1788 AGACAAAGCCAG 1847
Db 1563 GAGCGGAG 1622
Qy 1848 GAAAGACCTTTTGTGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1907
Db 1623 GAAAGATCTTTGTGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
Qy 1908 GAATATCATTAATCTTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1967
Db 1683 GAATATCATTAATCTTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1742
Qy 1968 GTATGCTTAAAG 2027
Db 1743 ATATGCTTCAAG 1802
Qy 2028 GTATGCTTAAAG 2087
Db 1803 GTATGCTTAAAG 1862
Qy 2088 ATGACACTTACAGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2147
Db 1863 TTGACAGTATCAAGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1922
Qy 2148 AGATTTAG 2207
Db 1923 GGAATTTAG 1982
Qy 2208 TGGAGTCCGAG 2267
Db 1983 TGGTTTGGGCGAG 2042
Qy 2268 TCCAGTCAAGTATGCTTCAAGAGCCCTGTTTGAATAGATATACACTATCAGATGA 2327
Db 2043 CCCGTAAGTATGATGCTTCAAGAGCCCTGTTTGAATAGATATACACTATCAGATGA 2102
Qy 2328 TGTCTGCTCTTCCGGGCTGTAAATGAGAGATCTTCACTTTAGGGGGCTCCCTACCC 2387
Db 2103 CGTCTGCTCTTCCGGGCTGTAAATGAGAGATCTTCACTTTAGGGGGCTCCCTACCC 2162

QY	2388	AGGATTTCCCGGTGGAGAACTTTTAAAGCTGCTGAAGAGACACACAAATGATTAAGC	2447
Db	2163	TGGATTTCACGTTGAAGAACTTTTCAAGTCTCTTAAAGGAGGCCACCAATGGACAAGCC	2222
QY	2448	AGCCAACTGCACCAACGAACTGATCATGTATGATGAAGGCACTGTTGGCATGCAAGAGCCCTC	2507
Db	2223	TGGCAACTGCACCAATGAGAGTGTATACAAATGATGAAGGCACTGCTGGCTGTGGCTTC	2282
QY	2508	CCAGAGCAACGCTCAAGAGTGGTAAAGACCTTGATCGAATTCCTACTCTCCACAC	2567
Db	2283	GCAAGACCCACTTTCAAGAGCTTTGTAGAGTCTAGACGGAATCTCAGCAAAAGCAC	2342
QY	2568	CAATGAGGAATCTTGGACCTCAGCCAACTCTCGAACAAGTATTCCTACTAGTTACCTGTA	2627
Db	2343	CAATGAGGAATCTTGGACCTCAGCCAACTCTGGAGCAGTACTGCCGACCTATCGGA	2402
QY	2628	CACAAAGATTTCTGTGTTCTTCAGAGATATTTCTGTTTTCTCCAGAGCCCAAGCCCTA	2687
Db	2403	TACCAAGAGTTCTGCTCTTTCTGGAGTATCTGTGTTCTTCTCCCGGAGCAATGGCCCTA	2462
QY	2688	CGAACATGCTTTCTCTCAGTATCAGACACAAATGAAGGCAAGCTGTTAAACATGA	2739
Db	2463	CGACCCCTGTCTTCCCAAAATCCCAACAGCAACGACACATTTAAACATGA	2514

```

RESULT 14
ID AA014848
AC AA014848 standard; DNA; 1603 BP.
XX
XX AA014848;
XX
DT 18-FEB-1992 (first entry)
XX
DE Clone PTB1228 encoding protein with FGF receptor activity.
XX
XX Human; fibroblast growth factor; cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 25..1602
FT /*tag= a
XX
XX MO9117183-A.
XX
XX 14-NOV-1991.
PD
XX
XX 25-APR-1991; 91WO-JP00557.
PF
XX
XX 28-DEC-1990; 90JP-0415801.
PR 27-APR-1990; 90JP-0113146.
PR 31-JUL-1990; 90JP-0204438.
PR 14-SEP-1990; 90JP-0245256.
XX
XX (TAKE ) TAKEDA CHEMICAL IND KK.
XX
XX Igarashi K, Senoo M, Watanabe T;
PI
XX WPI; 1991-353723/48.
DR
DR P-PSDB; AARI5266.
XX
XX New muten(s) of proteins - with fibroblast growth factor
PT receptor activity; useful for treating multiple endocrine
PT neoplasia, prostatic hypertrophy, used for diagnosis
XX
XX Example 2; Fig 3; 88bp; English.
XX
XX A cDNA library prepared from human cancer cell line Kato III mRNA
CC was screened with an oligonucleotide corresponding to amino acids
CC 539-541 of chicken basic FGF receptor. Three positive clones were
CC obtained. One was cloned into pUC118/119 to give pTB1228. The
CC nucleotide of pTB1228 is shorter than that of pTB1229 lacking
CC nucleotides 134-478 and 1309-1314 (see AA014849).

```

XX	Sequence
SQ	1603 BP; 434 A; 403 C; 441 G; 325 T; 0 other;

Query Match	30.9%	Score 1318.8;	DB 12;	Length 1603;
Best Local Similarity	94.7%;	Pred. No. 0;		
Matches 1404;	Conservative 0;	Mismatches 57;	Indels 21;	Gaps 3;

OY	728	GAGCACCACTACTGGACCAACACAGAAAAAGTGGAAAAAGCGGCTCCATGCTGTGCTTGGC	787
Db	134	GAGACACCATACTGTGACCCACACAGAAAAAGTGGAAAAAGCGGCTCCATGCTGTGCTTGGC	193
OY	788	CCAAACACTGTCAAATTTTCGCTGCCACAGCCGGGGGGAAACCAATTGCAACCAATTGGCGTGC	847
Db	194	CCAAACACTGTCAAATTTTCGCTGCCACAGCCGGGGGGAAACCAATTGCAACCAATTGCGGTGC	253
OY	848	TGAAAAACGGGAGAGATTTTAAGCAGAGCATTGCAATTGGAGGCTACAGGTACGAAACC	907
Db	254	TGAAAAACGGGAGAGATTTTAAGCAGAGCATTGCAATTGGAGGCTACAGGTACGAAACC	313
OY	908	AGCACTGGAGCTCTCAATTATGAGAAAGTGTGTCCACTGTACAGAGGAAATTAATACCTGTG	967
Db	314	AGCACTGGAGCTCTCAATTATGAGAAAGTGTGTCCACTGTACAGAGGAAATTAATACCTGTG	373
OY	968	TGTGTGAGAAATGAATACAGGGTCCCATCAATCACACGTACACCCTGGATGTGTGGAGCAT	1027
Db	374	TGTGTGAGAAATGAATACAGGGTCCCATCAATCACACGTACACCCTGGATGTGTGGAGCAT	433
OY	1028	CGCCTCACCGGCCCATCTCTCCAAAGCCGGACTGCCGGCAATGCTCTCCACAGTGTGCGAG	1087
Db	434	CGCCTCACCGGCCCATCTCTCCAAAGCCGGACTGCCGGCAATGCTCTCCACAGTGTGCGAG	493
OY	1088	GAGACGTAGATTTGTCTGCAAGGTTTACAGTATCCACAGCCCAATCCAGTGGATCA	1147
Db	494	GAGACGTAGATTTGTCTGCAAGGTTTACAGTATCCACAGCCCAATCCAGTGGATCA	553
OY	1148	AGCACGTGGAAAAAGACGCAATTAATACGGGCCGAGCGGCTGCCCTACCTCAAGTTTC	1207
Db	554	AGCACGTGGAAAAAGACGCAATTAATACGGGCCGAGCGGCTGCCCTACCTCAAGTTTC	613
OY	1208	TCAAGCGCGCGGGTGAACACACAGGACAAAGAGATTGAGTCTCTCATATTGTGGAAATG	1267
Db	614	TCAAGCACCTGGGGGATTAATTAATGTTCCAAATGCAAGTAGAGTGTGGCTCTGT-----TCAATG	667
OY	1268	TAACTTTTGAAGACGCTGGGGGAATATACGTGCTTGGCGGGTAATTCATTGGGATATCT	1327
Db	668	TGACCGAGCGGAGTGTGCTGGGGAATATATATATGTAAAGTCTCCAAATTATTAAGGCGAGGCA	727
OY	1328	TTCACTCTGCATGTTTACACAGTCTGCC-----ACGCGCTGGAAGAGAAAAAGGAGA	1378
Db	728	ACCAAGTCTGCTGGCTACGTCAGTCTCTGCTCCCAAAACAGCAACGCGCTGTGAAGAGAAAGGGA	787
OY	1379	TTTAAGCTTCCCACGACTACTCTGAGATAGCCATTTTACTGCTATAGGGGCTCTTCTTAATCG	1438
Db	788	TTTAAGCTTCCCACGACTACTCTGAGATAGCCATTTTACTGCTATAGGGGCTCTTCTTAATCG	847
OY	1439	CCTGTATGTGTGTAAACGTCATCTCTGTGCCGAATGAAGAACGACCAAGCCAGACT	1498
Db	848	CCTGTATGTGTGTAAACGTCATCTCTGTGCCGAATGAAGAACGACCAAGCCAGACT	907
OY	1499	TCAGAGAGCAGCGGGCTGTCCACAGGTGACCAAGCTAAAGCTATCCCGCTGGGGAGACAGGTAA	1558
Db	908	TCAGAGAGCAGCGGGCTGTCCACAGGTGACCAAGCTAAAGCTATCCCGCTGGGGAGACAG---	963
OY	1559	CAGTTTGGGCTAGTCCAGCTCCTCGCATGAACCTCAACACCCCGCTGTGTGAGGATTAACAA	1618
Db	964	--GTTTGGGCTAGATCCAGCTCCTCGCATGAACCTCAACACCCCGCTGTGTGAGGATTAACAA	1021
OY	1619	CAGCGCTCTCTTAAGAGGGAGACACCCCATGCTGGCAGGGGTCTCCGAGTATGAACCTTC	1678
Db	1022	CAGCGCTCTCTTAAGAGGGAGACACCCCATGCTGGCAGGGGTCTCCGAGTATGAACCTTC	1081
OY	1679	CAGAGGACCCCAAAATGGGACTTTTCCAAAGATTAAGCTGACATGTGGCAGAGCCCTGGGAG	1738

Db	1083	CAATTAATATTTGGGGAGGCCAACOCAGTCTCCGCTGCTCAOAGGTGCTGGCTGATCAGAGAA	1142
Qy	1368	-----AGAAAAGAGATTACAGCTTCCCGACAGTACCTGGAGATAGCCATTACTGCAT	1421
Db	1143	AGATGAAGAAGCGGAACACTGGATTCAATCAGGAGATACGGAAATCCGCATCTACTGCT	1202
Qy	1422	AGGGGCTCTCTTAATGGCCCTGATAGGTGTAACTCATCTCTGTGCCAATGAAAGAACAC	1481
Db	1203	GGGGAGCTTCTTATACCTCGCATGTATGTGGCAATCATGTGGTGTCCACATGAAAGGGGAG	1262
Qy	1482	GACCAAGAACCCAGACTTCAGCAGCGCCAGCGGCTGTGCACAAAGTGCACCAACGTATGCC	1541
Db	1263	AGGCAGAAAGTCTGACTTCAGCAGCGCCACCCGCTGTGCACAAAGCTGACAAAGATCTCCC	1322
Qy	1542	CTTGCGGAGACAGGTAAAGTTCGGGCTGATGTCAGCTCTTCATGAACCTCAACACCCC	1601
Db	1323	CTTGCGGAGACAGGTAAAGTTCGGGCTGATGTCAGCTCTTCATGAACCTCAACACCTCC	1382
Qy	1602	GCTGTGTAGGATTAACAACAGCCTCTCTTCAACGGCAGACACCCCATGCTGCGAGGGGT	1661
Db	1383	ACTGTGTCGGGATACACATCGCCTGTCTTCCAACATGATCACCCACTTGTCGGCGGGGT	1442
Qy	1662	CTCGGATATGAACCTTCAGAGGACCCAAATGGGGATTTCCAAAGATTAAGCTGACACT	1721
Db	1443	CTCGGATATGAGTCTGCCAGAGACCCCAAGTGGGAGTATCCAAAGGAAAGCTCACCT	1502
Qy	1722	GGGCAAGCCCCCTGGGAGAAAGTTCCTTTGGGCAAGTGGTGCATGGGCGAAGCAGTGGCAT	1781
Db	1503	GGGCAAGCCCCCTGGGAGAAAGTTCCTTTGGGCAAGTGGTGCATGGGCGAAGCGGTGGCAT	1562
Qy	1782	TGACAAAGACAGCCCAAGGAGCGGCTCACCGTGGCCGTGAAGATGTTGAAGATGATGC	1841
Db	1563	CGACAAAGACCGGCCAAAGATGTCACCGACCGTGGCAGTGAAGATGCTGAAGAAAGCAGTGC	1622
Qy	1842	CACAGAAAGACCTTTGATGATGTGTGCAGAGATGGAGATGATGAAGATGATGGGAA	1901
Db	1623	AACCGAAGAGATCTTCTTGATTTGGTGTGTGATGGAGAAATGAATGAATGATGGGAA	1682
Qy	1902	ACACAAAGATATCATTAATCTTCTTGAGACCTGCACACAGATGGGCCCTCTCTATGTGAT	1961
Db	1683	GCATAAAGATATCATCAATCTTGTAGAGCGTGCACCCAAAGATGGCCCATCTCACTGAT	1742
Qy	1962	AGTTGATATGCTCTTAAGGCAACTCCGAGAAATACCTCGAGCCCGGAGGCCACCCGG	2021
Db	1743	AGTGAATATGCTCCAAAGGGGAACCTTGGTGAATACCTTGCACACCCGCCACACTGG	1802
Qy	2022	GATGAGATACCTCCTATGACATTAAACGCTGTCTCTAGAGAGCAGATGACTTCAAGATTT	2081
Db	1803	CATGAGATACCTCCTTGTACATCAACAGAAATTCCTTGAAAGCAGATGACTTCAAGACTT	1862
Qy	2082	GGTGTATGACCTACACAGCTGCGCCAGAGCGATGAGTACTTGGCTTCCCAAAAATGTAT	2141
Db	1863	AGTGTCTTTCAGACTACCAAGTGGCCAGGGGAATGAGTACTCTGGCATACAGAAAGTGCAT	1922
Qy	2142	TCATCGAGATTTAGCAGCCGAAATGTTTGGTAAACAGAAAAAATGTGATGATAAATAGC	2201
Db	1923	CCATCGGAGACTTGGACACTGGGAATCTTGTGGAGCAAGAACCAACGTCATGAAAAATGTC	1982
Qy	2202	AGACTTTGAGACTCGCCAGAGATATCAACAATATAGACTTTTCAAAAAAGACCACCAATGG	2261
Db	1983	AGATTTTGGTTTGGCCCGAGACATCAACAACATCGACTCTCAAAAAAACCAACCAAGG	2042
Qy	2262	GGGCTTTCACAGTCAAGTGAATGCGCTCCAGAGGCGCTTGTATAGAGTATACACTCATCA	2321
Db	2043	CCGGCTCCCGGTGAAGTGAATGCGCTCCCGAGGCGCTTGTGACAGAGTCTTACACATCA	2102
Qy	2322	GAGTGATGTCTGTCTTTCGGGGGTGTTAATGTGGAGATCTTCACTTTAAGGGGCGCTGCC	2381
Db	2103	GAGTGAAGCTGTGGCTTTCGGTGTGTTATGTGGAGATCTTCAACACTGGGGGTTTCCC	2162
Qy	2382	CTACCAGGAGATTCGCTGGAGAACTTTTAAAGTGTCTGAAGGAAGACACAGAAATGGA	2441

Db	2163	ATACCTGGAAATTCAGTTGGAAGACTTTTTCAAAGCTCCCTTAAAGGAAGGCCACCAAGATGGA	2222
Qy	2442	TAAACCCAGCCAACTGCACCCACCAACTGTTCATGATGATGAGGAGACTGTTGGCATGCACT	2501
Db	2223	CAACCTCGGACATGCAACCATATAGTGTATACAAATGAATGAGACGAGCTGCTGGCGTGTGT	2283
Qy	2502	GCCCTCCAGAGACCAACGTCCTCAAGCATGTTGTGTAGAGAAGCTTGAGATGCATTCCTACTCT	2561
Db	2283	GCCCTCGCAAGAAGCCCACTTTCAAAGCAGGCTGTGTGAGATCTTAGACCCGATCCTCAGCA	2342
Qy	2562	CACACCAATGAGGAATACCTTGGACCTCAGCCACTCTTCGAACGATATTAACCTAGTTA	2621
Db	2343	AAGACCAATGAGGAGATACCTGGAACCTCAACAACCTCTGGAGCAGTACTCCCGAGCTA	2402
Qy	2622	CCCTGCACACAAGATGTCCTGTCTTCAGAGAGATGATTCGTTTTTCTCCAGACCCAT	2681
Db	2403	TCCGATATCCAGGAGTTCCTGCTCTTCTGGGAGTAGCTGTCTTCTCCCGGAGCAAT	2462
Qy	2682	GCCTTACGAACATGCGCTTCTCTAGATATCCACACATAAACGGCAGTGTTAAACATGA	2739
Db	2463	GCCCTACGACCCCTGCTTCTCCCAAAATCCCAACACACAAAGGACCATTAATAAACATGA	2520

Search completed: December 11, 2002, 14:31:24
Job time : 598 secs

Job time : 598 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:57:41 ; Search time 99 Seconds
(without alignments)
13221.176 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 cccaagaccactctcttcg.....actaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCFUS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/Backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3386.6	79.3	3416	2 US-08-451-822A-15	Sequence 15, Appl
2	3386.6	79.3	3416	4 US-08-323-430-15	Sequence 15, Appl
3	2191.2	51.3	2676	1 US-08-471-570-7	Sequence 7, Appl
4	1817.2	42.6	1954	1 US-08-471-570-5	Sequence 5, Appl
5	1692.8	39.7	2310	1 US-08-471-570-9	Sequence 9, Appl
6	1367.6	32.0	2675	1 US-08-070-165F-5	Sequence 5, Appl
7	1367.6	32.0	2675	2 US-08-885-418-5	Sequence 5, Appl
8	1318.8	30.9	1603	1 US-08-471-570-3	Sequence 3, Appl
9	1276.4	29.9	2681	1 US-08-070-165F-9	Sequence 9, Appl
10	1276.4	29.9	2681	2 US-08-885-418-9	Sequence 9, Appl
11	1182.2	27.7	2469	1 US-07-997-133-2	Sequence 2, Appl
12	1182.2	27.7	2469	5 US-08-459-296-1	Sequence 5, Appl
13	1182.2	27.7	2469	5 US-07-997-133-2	Sequence 2, Appl
14	1180.6	27.7	2662	2 US-08-451-822A-14	Sequence 14, Appl
15	1180.6	27.7	2662	4 US-08-323-430-14	Sequence 14, Appl
16	1159.2	27.2	2733	1 US-08-371-001-14	Sequence 14, Appl
17	1159.2	27.2	2733	5 PCT-US93-06031-14	Sequence 14, Appl
18	1141	26.7	3503	1 US-07-631-717A-1	Sequence 1, Appl
19	1141	26.7	3503	1 US-08-166-717D-1	Sequence 1, Appl
20	981.8	23.0	5993	4 US-09-383-630-1	Sequence 1, Appl
21	981.8	23.0	5993	4 US-09-383-630-2	Sequence 2, Appl
22	961.8	22.5	2049	4 US-09-099-748-10	Sequence 10, Appl
23	956.2	22.4	8083	4 US-09-383-630-4	Sequence 4, Appl
24	956.2	22.4	8083	4 US-09-383-630-5	Sequence 5, Appl
25	931.6	21.8	1079	1 US-08-471-570-13	Sequence 13, Appl
26	623.2	14.6	1875	1 US-08-070-165F-3	Sequence 3, Appl
27	623.2	14.6	1875	2 US-08-885-418-3	Sequence 3, Appl

28	623	14.6	1839	1 US-08-070-165F-7	Sequence 7, Appl
29	623	14.6	1839	2 US-08-885-418-7	Sequence 7, Appl
30	603.4	14.1	605	1 US-08-471-570-1	Sequence 1, Appl
31	598.8	14.0	1056	2 US-08-701-191A-5	Sequence 5, Appl
32	597.6	14.0	933	2 US-08-701-191A-4	Sequence 4, Appl
33	542.2	12.7	734	1 US-08-471-570-11	Sequence 11, Appl
34	426.2	10.0	1983	4 US-09-057-860A-8	Sequence 8, Appl
35	245.4	5.7	4508	5 PCT-US93-06251-34	Sequence 34, Appl
36	205	4.8	4138	1 US-08-323-474-1	Sequence 1, Appl
37	205	4.8	4138	1 PCT-US93-06093-1	Sequence 1, Appl
38	197.4	4.6	360	5 PCT-US93-05703-1	Sequence 1, Appl
39	194	4.5	3845	2 US-08-220-240A-4	Sequence 4, Appl
40	192.8	4.5	5406	1 US-07-813-593-3	Sequence 3, Appl
41	192.8	4.5	5406	1 US-07-977-451-5	Sequence 5, Appl
42	192.8	4.5	5406	1 US-07-946-507-3	Sequence 3, Appl
43	192.8	4.5	5406	1 US-08-252-517-5	Sequence 5, Appl
44	192.8	4.5	5406	1 US-07-906-397A-5	Sequence 5, Appl
45	192.8	4.5	5406	1 US-08-601-891-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-451-822A-15
Sequence 15, Application US/08451822A
Patent No. 5863888
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 05-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-08-451-822A-15

Query Match	79.3%;	Score 3386.6;	DB 2;	Length 3416;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 3411;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 2;
QY 93 CAGAGTGGGGAGGCGCTTGGCATTCAGAGTGCAGCAGCAGGAGCGGCGG 152				
Db 2 CCGAGTCCGGGAGAGCCGTTGCCATTCAAGTACAGCAGCAGCAGCGGCGG 60				
QY 153 TTCTCTAGGCCAGCCGAGCGCTGAAGCATTCGCCGTAGTCATGCGCGTAAGAGAGTGT 212				
Db 61 TTCTCTAGGCCAGCCGAGCGCTGAAGCATTCGCCGTAGTCATGCGCGTAAGAGTGT 119				
QY 213 GCAGATGGGATTACGTCACATGAGATATGGAAGAGAGCCGGGATTTGGTACCGTAAC 272				
Db 120 GCAGATGGGATTACGTCACATGAGATATGGAAGAGAGCCGGGATTTGGTACCGTAAC 179				
QY 273 CATGTCAGCTGGGGTGTTCATCTGCGTGGTGTGTCACCATGGCAACTGTCCCT 332				
Db 180 CATGTCAGCTGGGGTGTTCATCTGCGTGGTGTGTCACCATGGCAACTGTCCCT 239				
QY 333 GGGCCGGCCCTCTTCAATTAGTGAAGATTCACATTAGAGCCAGAGAGCCACCAAC 332				
Db 240 GGGCCGGCCCTCTTCAATTAGTGAAGATTCACATTAGAGCCAGAGAGCCACCAAC 299				
QY 393 CAATATCAAAATCTCTCAACCAAGTGTACGTGGCTGGCCAGGGGAGTGCCTAGAGT 452				
Db 300 CAATATCAAAATCTCTCAACCAAGTGTACGTGGCTGGCCAGGGGAGTGCCTAGAGT 359				
QY 453 GCGCTGCTTTGAAGATGCCCGCGTATCAGTTGGACTAAGAGTGGGTGACTTGGG 512				
Db 360 GCGCTGCTTTGAAGATGCCCGCGTATCAGTTGGACTAAGAGTGGGTGACTTGGG 419				
QY 513 GCCCAACATAGACAGTCTTATTTGGGAGTACTTGCAGATAAAGGGCCGACGCTTAG 572				
Db 420 GCCCAACATAGACAGTCTTATTTGGGAGTACTTGCAGATAAAGGGCCGACGCTTAG 479				
QY 573 AGACTCGGCGCTTATGCTGTACTGCGCACTAGAGACTGTAGACAGTGAACCTTGGTACTT 632				
Db 480 AGACTCGGCGCTTATGCTGTACTGCGCACTAGAGACTGTAGACAGTGAACCTTGGTACTT 539				
QY 633 CATGTGAATGTCAACAGATCCATCTTCATCCGAGATGATGAGATGACACCGATGGTC 692				
Db 540 CATGTGAATGTCAACAGATCCATCTTCATCCGAGATGATGAGATGACACCGATGGTC 599				
QY 693 GGAAGATTTTGTCAAGTGAAGACATCAACAAGAGAGCAACCATCTGAGCAACACAGA 752				
Db 600 GGAAGATTTTGTCAAGTGAAGACATCAACAAGAGAGCAACCATCTGAGCAACACAGA 659				
QY 753 AAGATGGAAGAGCGCTCATGCTGTGCTGGCCACACAGTCAAGTTTGGTGGCC 812				
Db 660 AAGATGGAAGAGCGCTCATGCTGTGCTGGCCACACAGTCAAGTTTGGTGGCC 719				
QY 813 AGCGGGGGGAAACCCCAATGCGCAACCATGCGGTGGGTAAGGAGGGAAGGTTTAAACA 872				
Db 720 AGCGGGGGGAAACCCCAATGCGCAACCATGCGGTGGGTAAGGAGGGAAGGTTTAAACA 779				
QY 873 GGAAGATGGAAGAGCGCTCATGCTGTGCTGGCCACACAGTCAAGTTTGGTGGCC 932				
Db 780 GGAAGATGGAAGAGCGCTCATGCTGTGCTGGCCACACAGTCAAGTTTGGTGGCC 839				
QY 933 TGTGTGCTCCATGTGACAAAGGAAATTTATACCTGTGTGTGAGAAATGAATACGGGTCCAT 992				
Db 840 TGTGTGCTCCATGTGACAAAGGAAATTTATACCTGTGTGTGAGAAATGAATACGGGTCCAT 899				
QY 993 CAATACACAGTACACCTGTGATGTTGTGAGCATGCGCTACCGGCGCATCTCCCAAGC 1052				
Db 900 CAATACACAGTACACCTGTGATGTTGTGAGCATGCGCTACCGGCGCATCTCCCAAGC 959				
QY 1053 CGGACTGCGCGCAAAATGCCCTTCACAGTGTGGGAGGAGGTAGAGTTTGTCTGCAAGGT 1112				
Db 960 CGGACTGCGCGCAAAATGCCCTTCACAGTGTGGGAGGAGGTAGAGTTTGTCTGCAAGGT 1019				

QY 1113 TTACATGATGCCACACCCACATCCAGTGSATTCAGACAGCTGGAAGAAAGCGCATAA 1172				
Db 1020 TTACATGATGCCACACCCACATCCAGTGSATTCAGACAGCTGGAAGAAAGCGCATAA 1079				
QY 1173 ATACGGGCCGAGAGGGCTCCCTACCTCAAGGTTTCAAGGCGCGGTTTAAACACAC 1232				
Db 1080 ATACGGGCCGAGAGGGCTCCCTACCTCAAGGTTTCAAGGCGCGGTTTAAACACAC 1139				
QY 1233 GGAACAAAGATTTAGGTTCTCTATATTTGGAATGTAATCTTTTGAAGACCTTGGGAAATA 1292				
Db 1140 GGAACAAAGATTTAGGTTCTCTATATTTGGAATGTAATCTTTTGAAGACCTTGGGAAATA 1199				
QY 1293 TACGCTTTGGGGGTAATTTCTATTGGGATTCCTTCACTGCTGATGGTTGACATTTCT 1352				
Db 1200 TACGCTTTGGGGGTAATTTCTATTGGGATTCCTTCACTGCTGATGGTTGACATTTCT 1259				
QY 1353 GCCAGCCCTGGAAGAGAAAGAGATTACAGCTTCCAGACTACCTGAGATAGCAT 1412				
Db 1260 GCCAGCCCTGGAAGAGAAAGAGATTACAGCTTCCAGACTACCTGAGATAGCAT 1319				
QY 1413 TTACTGATAGGGGTTCTTTAATGCGCTGTATGTGTATACAGTATCTCTGTGCCAAT 1472				
Db 1320 TTACTGATAGGGGTTCTTTAATGCGCTGTATGTGTATACAGTATCTCTGTGCCAAT 1379				
QY 1473 GAAGAACAGGACCAAGAACGACATTCAGACAGCCAGCGGGGTGACACAGCTGACCA 1532				
Db 1380 GAAGAACAGGACCAAGAACGACATTCAGACAGCCAGCGGGGTGACACAGCTGACCA 1439				
QY 1533 ACCTATCCCTCCGAGAGACAGTAACTTTCGCGTGAAGTCCAGCTCTCATAGACTC 1592				
Db 1440 ACCTATCCCTCCGAGAGACAGTAACTTTCGCGTGAAGTCCAGCTCTCATAGACTC 1499				
QY 1593 CAACACCCGCTGTGAGGATTAACAACAGCCCTCTCTTCAAGGGCAGACACCCCATGCT 1652				
Db 1500 CAACACCCGCTGTGAGGATTAACAACAGCCCTCTCTTCAAGGGCAGACACCCCATGCT 1559				
QY 1653 GGCAGGGGTCTCCGATATGAACTTCAGAGAGACCCAAATGGAGTTTCAAGAGATTA 1712				
Db 1560 GGCAGGGGTCTCCGATATGAACTTCAGAGAGACCCAAATGGAGTTTCAAGAGATTA 1619				
QY 1713 GCTGACACTGCGGAGGCGCTTGGGAGAGTTCCTTTGGCAAGTGTATGGCGGAGC 1772				
Db 1620 GCTGACACTGCGGAGGCGCTTGGGAGAGTTCCTTTGGGCAAGTGTATGGCGGAGC 1679				
QY 1773 AGTGGGAATTTGACAAAGACAAAGCCCAAGGAGGCGGTACACGCTGGCGGTGAAGTGTGAA 1832				
Db 1680 AGTGGGAATTTGACAAAGACAAAGCCCAAGGAGGCGGTACACGCTGGCGGTGAAGTGTGAA 1739				
QY 1833 AGATGATGCCACAGAGAAAGACCTTTCGTATCTGTGTGATGAGATGAGATGAAAT 1892				
Db 1740 AGATGATGCCACAGAGAAAGACCTTTCGTATCTGTGTGATGAGATGAGATGAAAT 1799				
QY 1893 GATTGGAAACACAGAAATATCAATAATCTTTGAGAGCTTGCACACAGAGATGGCTCT 1952				
Db 1800 GATTGGAAACACAGAAATATCAATAATCTTTGAGAGCTTGCACACAGAGATGGCTCT 1859				
QY 1953 CTATGTCATGTTGAGATGCGCTAAAGGCAACCTCCGAATTAACCTCGAGCCGGAG 2012				
Db 1860 CTATGTCATGTTGAGATGCGCTAAAGGCAACCTCCGAATTAACCTCGAGCCGGAG 1919				
QY 2013 GCCACCCGGGATGAGTACTCTATGACATTAACCGTGTCTTGAGAGAGAGATGACCTT 2072				
Db 1920 GCCACCCGGGATGAGTACTCTATGACATTAACCGTGTCTTGAGAGAGAGATGACCTT 1979				
QY 2073 CAAGGACTTGGTCTCATGACCTTACAGAGCTGCGCAGAGGATGAGTACTTGGCTTCCA 2132				
Db 1980 CAAGGACTTGGTCTCATGACCTTACAGAGCTGCGCAGAGGATGAGTACTTGGCTTCCA 2039				
QY 2133 AAAATGATTCATGAGATTTAGCAGCGCAAAATGTTTGTGTAACAGAAACAAATGTGAT 2192				
Db 2040 AAAATGATTCATGAGATTTAGCAGCGCAAAATGTTTGTGTAACAGAAACAAATGTGAT 2099				

|||||
Db 61 TTCTCAGGCCACCGCA-GCTGAAAGCATGGCGGTAGTCATGCCGTAAGAAAGTGT 119
Oy 213 GCAGATGGGATTAACGTCCACATGGAGATATGAAAGAGACCGGGATTTGTACCTAAC 272
Db 120 GCAGATGGGATTAACGTCCACATGGAGATATGAAAGAGACCGGGATTTGTACCTAAC 179
Oy 273 CATGTGCACGTGGGTGCTTTCATCTGCGTGTGCTGCTCACCATTGGCAACCTTGTCCCT 332
Db 180 CATGTGCACGTGGGTGCTTTCATCTGCGTGTGCTGCTCACCATTGGCAACCTTGTCCCT 239
Oy 333 GGGCCGGCCCTCTTCAAGTTTAACTTGAAGATACACATTAGAGCCGAAAGAGCCACCAAC 392
Db 240 GGGCCGGCCCTCTTCAAGTTTAACTTGAAGATACACATTAGAGCCGAAAGAGCCACCAAC 299
Oy 393 CAAATACCAATCTCAACACGAACTGTAAGTGGTGGCCGAGGGGAGTCCCTTAAGCT 452
Db 300 CAAATACCAATCTCAACACGAACTGTAAGTGGTGGCCGAGGGGAGTCCCTTAAGCT 359
Oy 453 GCGCTGCTGTTGAAAGATGCCGCGTGTATCAAGTTGACTAAGAGATGGGGTGCATTTGG 512
Db 360 GCGCTGCTGTTGAAAGATGCCGCGTGTATCAAGTTGACTAAGAGATGGGGTGCATTTGG 419
Oy 513 GCCCAACAATAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGGCCACGCTTAG 572
Db 420 GCCCAACAATAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGGCCACGCTTAG 479
Oy 573 AGACCTGGGCTCTATGCTTGTACTGCGAGTAGAGTGAACAGTGAACCTTGTACTT 632
Db 480 AGACCTGGGCTCTATGCTTGTACTGCGAGTAGAGTGAACAGTGAACCTTGTACTT 539
Oy 633 CATGTGAATGTCAACAGATGCCATCTCATCCGAGATGATGAGATGACACCGATGGTC 692
Db 540 CATGTGAATGTCAACAGATGCCATCTCATCCGAGATGATGAGATGACACCGATGGTC 599
Oy 693 GGAAGATTTTGTACGTAGAACAGTAAACAAGAGACCATTAAGTGAACACAGTAA 752
Db 600 GGAAGATTTTGTACGTAGAACAGTAAACAAGAGACCATTAAGTGAACACAGTAA 659
Oy 753 AAGATGGAAGAGCGGCTCATGCTGCTGGCGGCAACAGTGTCAAGTTTGGCTGCC 812
Db 660 AAGATGGAAGAGCGGCTCATGCTGCTGGCGGCAACAGTGTCAAGTTTGGCTGCC 719
Oy 813 AGCGGGGGGAACCCAAATGCCAATGCCGCTGTAAGAAAACGGGAGAGTTTAAAGA 872
Db 720 AGCGGGGGGAACCCAAATGCCAATGCCGCTGTAAGAAAACGGGAGAGTTTAAAGA 779
Oy 873 GGAAGATTTTGTACGTAGAACAGTAAACAAGAGACCATTAAGTGAACACAGTAA 932
Db 780 GGAAGATTTTGTACGTAGAACAGTAAACAAGAGACCATTAAGTGAACACAGTAA 839
Oy 933 TGTGCTCCATCTGACAAAGGAAATTAATCTGTGTGTGAGAGAAATGAGGGTCAAT 992
Db 840 TGTGCTCCATCTGACAAAGGAAATTAATCTGTGTGTGAGAGAAATGAGGGTCAAT 899
Oy 993 CAATCAGACGTACACACTGGATTTGTGAGAGATGCCCTCACCGGCCCATCTCCAAAC 1052
Db 900 CAATCAGACGTACACACTGGATTTGTGAGAGATGCCCTCACCGGCCCATCTCCAAAC 959
Oy 1053 CGGACTGCGGCAAAATGCTCCACAGTGTGCGAGAGAGAGTGAAGTTGTCTGCAAGT 1112
Db 960 CGGACTGCGGCAAAATGCTCCACAGTGTGCGAGAGAGAGTGAAGTTGTCTGCAAGT 1019
Oy 1113 TTACAGTGAATGCCACCGCACATCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1172
Db 1020 TTACAGTGAATGCCACCGCACATCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1079
Oy 1173 ATACGGGGCCGAGAGGCTCCCTCAAGTGTCTCAAGGCGCGGCTTGAACACCAAC 1232
Db 1080 ATACGGGGCCGAGAGGCTCCCTCAAGTGTCTCAAGGCGCGGCTTGAACACCAAC 1139
Oy 1233 GGAACAAGATTTGAGGTTCTATATTTGGAATGTAACTTTTGAAGACGCTGGGGAATA 1292
|||||

Db 1140 GGAACAAGATTTGAGGTTCTATATTTGGAATGTAACTTTTGAAGACGCTGGGGAATA 1199
Oy 1293 TACGTCTTGGCGGCTTAATTTATTTGGGATATCCCTTTCACCTCTGCATGGTTGACATTTCT 1352
Db 1200 TACGTCTTGGCGGCTTAATTTATTTGGGATATCCCTTTCACCTCTGCATGGTTGACATTTCT 1259
Oy 1353 GCCAGCGCTGGAAGAGAAAGAGATTAACAGTTCGCCAGACTACCTGGAGATAGCCAT 1412
Db 1260 GCCAGCGCTGGAAGAGAAAGAGATTAACAGTTCGCCAGACTACCTGGAGATAGCCAT 1319
Oy 1413 TTATGCTATAGGGGCTTCTTAAATGCCCTGTATGTGTGTATGATATGATATGATATGAT 1472
Db 1320 TTATGCTATAGGGGCTTCTTAAATGCCCTGTATGTGTGTATGATATGATATGATATGAT 1379
Oy 1473 GAAAGACAGACCAAGAACGACACTTACAGAGCCGCGGCTGTGCACAGCTGACCAA 1532
Db 1380 GAAAGACAGACCAAGAACGACACTTACAGAGCCGCGGCTGTGCACAGCTGACCAA 1439
Oy 1533 ACCTATCCCTGCGGAGACAGTAACTTCCGCTGAGTCCAGCTCCCTCATGAACTC 1592
Db 1440 ACCTATCCCTGCGGAGACAGTAACTTCCGCTGAGTCCAGCTCCCTCATGAACTC 1499
Oy 1593 CAACACCCGCTGTGTAGAGATTAACAACACGCTCTCTTCAAGGCGAGACACCCCATGCT 1652
Db 1500 CAACACCCGCTGTGTAGAGATTAACAACACGCTCTCTTCAAGGCGAGACACCCCATGCT 1559
Oy 1653 GCGAGGGGTCTCCGATTAAGAACTTCCAGAGACCCAAATGGGAGTTTCAAGATATA 1712
Db 1560 GCGAGGGGTCTCCGATTAAGAACTTCCAGAGACCCAAATGGGAGTTTCAAGATATA 1619
Oy 1713 GCTGACACTGGGCAACCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTATGGCGGAAC 1772
Db 1620 GCTGACACTGGGCAACCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTATGGCGGAAC 1679
Oy 1773 AGTGGGAATTTGACAAAGACAAAGCCCAAGAGCGGCTCACCGTGGCGGTGAAGTTGTA 1832
Db 1680 AGTGGGAATTTGACAAAGACAAAGCCCAAGAGCGGCTCACCGTGGCGGTGAAGTTGTA 1739
Oy 1833 AGATGATGCGCACAGAAAGACCTTCTGATGCTGTGTGAGAGATGAGATGATGAAGAT 1892
Db 1740 AGATGATGCGCACAGAAAGACCTTCTGATGCTGTGTGAGAGATGAGATGATGAAGAT 1799
Oy 1893 GATTTGGAAACACAAAGATATCAATAATCTTCTTGGAGCCTGCACACAGATGGGCTCT 1952
Db 1800 GATTTGGAAACACAAAGATATCAATAATCTTCTTGGAGCCTGCACACAGATGGGCTCT 1859
Oy 1953 CTATGCTATAGTTGATATGCTCTTAAGGCAACCTCCAGAAATTAACCTCCGAGCCGGAG 2012
Db 1860 CTATGCTATAGTTGATATGCTCTTAAGGCAACCTCCAGAAATTAACCTCCGAGCCGGAG 1919
Oy 2013 GCCACCCGGGATGGAATTAACCTCTATGACATTAACCTGTTCCGTGAGAGACAGATGACCTT 2072
Db 1920 GCCACCCGGGATGGAATTAACCTCTATGACATTAACCTGTTCCGTGAGAGACAGATGACCTT 1979
Oy 2073 CAAGACTTGTGTATGACACCTTACAGCTGGCCAGAGGATGAGTACTTGGCTTCCCA 2132
Db 1980 CAAGACTTGTGTATGACACCTTACAGCTGGCCAGAGGATGAGTACTTGGCTTCCCA 2039
Oy 2133 AAAATATTTATGACGATTTTGAAGCCGAAATGTTTTGTGTAAAGAAACAAATGTGAT 2192
Db 2040 AAAATATTTATGACGATTTTGAAGCCGAAATGTTTTGTGTAAAGAAACAAATGTGAT 2099
Oy 2193 GAAATATGACGATTTTGAAGCTGGCCAGAAATTAACCAATATTAAGTATTAAGAAAGAC 2252
Db 2100 GAAATATGACGATTTTGAAGCTGGCCAGAAATTAACCAATATTAAGTATTAAGAAAGAC 2159
Oy 2253 CACCAATGGGCGGCTTCCAGTCAAGTGCATGCTCCAGAGCCCTTGTGATAGATATA 2312
Db 2160 CACCAATGGGCGGCTTCCAGTCAAGTGCATGCTCCAGAGCCCTTGTGATAGATATA 2219
Oy 2313 CACTCATCAGAGTATGCTGTGCTCTTCCGGGCTTTAAATGTGGAGATCTTCACTTAGG 2372
Db 2220 CACTCATCAGAGTATGCTGTGCTCTTCCGGGCTTTAAATGTGGAGATCTTCACTTAGG 2279
|||||

OY	2373	GGGCTGGCCCTACCCAGGAGATCCCGGAGGAACTTTTAAAGCTGCGTAAGCAGAGACA	2433
Db	2280	GGGCTGGCCCTACCCAGGAGATCCCGGAGGAACTTTTAAAGCTGCGTAAGCAGAGACA	2339
OY	2433	CAGAAATGGAATAGCCACGCAACTGTGCACCAACGAACTGTACATGATGATGAGGACTGTTG	2492
Db	2340	CAGAAATGGAATAGCCACGCAACTGTGCACCAACGAACTGTACATGATGATGAGGACTGTTG	2399
OY	2493	GCATGCAAGTGGCCCTCCGAGAGACCAACGTTCAACGAGTGGTATGAAAGACTTGGATCGAAT	2553
Db	2400	GCATGCAAGTGGCCCTCCGAGAGACCAACGTTCAACGAGTGGTATGAAAGACTTGGATCGAAT	2459
OY	2553	TCTGACTCTGCACAACCAATGAGGAATACCTTGGACCTCAGCCAACTCTCGAACACTATTC	2612
Db	2460	TCTGACTCTGCACAACCAATGAGGAATACCTTGGACCTCAGCCAACTCTCGAACACTATTC	2519
OY	2613	ACCTAGTTACCCCTGACACCAAGAAGTCTTGTTCTTGTAGAGATGATTCGTGTTTTCTCC	2672
Db	2520	ACCTAGTTACCCCTGACACCAAGAAGTCTTGTTCTTGTAGAGATGATTCGTGTTTTCTCC	2579
OY	2673	AGACCCCATGCTCTACGAAACCATGCGCTCCCTCGATGTCACACATAAACGGAGGTAA	2732
Db	2580	AGACCCCATGCTCTACGAAACCATGCGCTCCCTCGATGTCACACATAAACGGAGGTAA	2639
OY	2733	AACATGAATGACTGTGTCTGCTGTCCTCCCAACAGACAGCACTGGGAACCTAGCTACAC	2792
Db	2640	AACATGAATGACTGTGTCTGCTGTCCTCCCAACAGACAGCACTGGGAACCTAGCTACAC	2699
OY	2793	TGACACGAGGAGACCATGCGCTCCCTCGATGTCACACATAAACGGAGGTAA	2852
Db	2700	TGACACGAGGAGACCATGCGCTCCCTCGATGTCACACATAAACGGAGGTAA	2759
OY	2853	GAGTAAATTAATTGGAAAAAGTAATCAGCATATGTGTAAACATTTATACAGTTGAAACCTTG	2912
Db	2760	GAGTAAATTAATTGGAAAAAGTAATCAGCATATGTGTAAACATTTATACAGTTGAAACCTTG	2819
OY	2913	TAAATCTCCCCAGAGAGAGAAAGGTTTCTGGAGCAGTGGACTGCCAACCCACCATG	2972
Db	2820	TAAATCTCCCCAGAGAGAGAAAGGTTTCTGGAGCAGTGGACTGCCAACCCACCATG	2879
OY	2973	TAAACCTCTCACCTGGCGGCTTCTGGCTGTGGACACAGTGAAGCTGAAGGTGAGCTG	3032
Db	2880	TAAACCTCTCACCTGGCGGCTTCTGGCTGTGGACACAGTGAAGCTGAAGGTGAGCTG	2939
OY	3033	CGTTCTGCCCTCTCTGTTAAATTTTGTAAATTAATTTGAGAAAGATTTATGTACACACACTT	3092
Db	2940	CGTTCTGCCCTCTCTGTTAAATTTTGTAAATTAATTTGAGAAAGATTTATGTACACACACTT	2999
OY	3093	ACAGAGCACAAAATGCAAGTATATAGGAGGCGGAAATGTAATGTAATATATCAAAATATATGAT	3152
Db	3000	ACAGAGCACAAAATGCAAGTATATAGGAGGCGGAAATGTAATGTAATATATCAAAATATATGAT	3059
OY	3153	AAATATATTAATATATATTTACAAGAGATATTTTGTATTGATTTTAAATGCAAGTGTCC	3212
Db	3060	AAATATATTAATATATATTTACAAGAGATATTTTGTATTGATTTTAAATGCAAGTGTCC	3119
OY	3213	AATGCACTTGAAGAAATTTGGCTCTCTTTTTTAAATAGCTATTTGCTAAATGCTGTTCTTA	3272
Db	3120	AATGCACTTGAAGAAATTTGGCTCTCTTTTTTAAATAGCTATTTGCTAAATGCTGTTCTTA	3179
OY	3273	CACATTAATTTCTTAATTTTACCGCAGACAGAGTGGAAAAATCTTTGCTTCAGGGGAAA	3332
Db	3180	CACATTAATTTCTTAATTTTACCGCAGACAGAGTGGAAAAATCTTTGCTTCAGGGGAAA	3239
OY	3333	ATGATTAATACGTTAAATTTATTAATTAATTTGTTATATACAAAACAAATTAATCATTTATAG	3392
Db	3340	ATGATTAATACGTTAAATTTATTAATTAATTTGTTATATACAAAACAAATTAATCATTTATAG	3299
OY	3393	TTTTTTTTTGAATTTTAAGGGCAATTTCTATGAGAGCAGACAGCACTAGTTAATCTAT	3452
Db	3300	TTTTTTTTTGAATTTTAAGGGCAATTTCTATGAGAGCAGACAGCACTAGTTAATCTAT	3359

[illegible]

RESULT 3
US-08-471-570-7

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

? COMPUTER READABLE FORM:
?
? MEDIUM TYPE: Floppy disk
?
? COMPUTER: IBM PC compatible
?
? OPERATING SYSTEM: PC-DOS/MS-DOS
?
? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:

```

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	51.3%	Score 2191.2	DB 1	Length 2676
Best Local Similarity	96.9%	Pred. No. 0		
Matches 2261	Conservative	0	Mismatches 58	Indels 15
				Gaps 2

QY	250	GGACCGGGGATTTGGTAACGTATACCAAGGTGACGAGGGTGTGTTTCACTGCTGTGCTG	305
Db	1	GGACCGGGGATTTGGTACCGTATACCAATGTCACGCTGGGTCCTTCACTGCTGTGCTG	60
QY	310	GTCACACATGGCAACCTTGTCCCTGTCCGCGCGCCCTCTTCAAGTTAGTTGAGGATACCA	365
Db	61	GTCACACATGGCAACCTTGTCCCTGTCCCTGTCCGCGCGCCCTCTTCAAGTTAGTTGAGGATACCA	120
QY	370	TTAGAGCAGAGAAGCCACCAACCAAAATATACCAAAATCTCTCAACCAAGAAGTGTACGTGGCT	425
Db	121	TTAGAGCAGAGAAGCCACCAACCAAAATATACCAAAATCTCTCAACCAAGAAGTGTACGTGGCT	180

OY	430	GCGCCAGGGAGTGGCTAGAGAGTGGCCCTGCTGTGGAAAGATGCCGCCGTATCAGTTGG	489
Db	181	GCGCCAGGGAGTGGCTAGAGAGTGGCCCTGCTGTGGAAAGATGCCGCCGTATCAGTTGG	240
OY	490	ACTAAGAGTGGGGTGCCTTGGGGGCCCAACAAATAGACAGTGTCTTAATTTGGGAGTACTTG	549
Db	241	ACTAAGAGTGGGGTGCCTTGGGGGCCCAACAAATAGACAGTGTCTTAATTTGGGAGTACTTG	300
OY	550	CAGATTAAGGGCGCCAGCAGCCTTAGAGACTCCGGGCTCTTAAGCTTGTACTGCCAGTAGAGACT	609
Db	301	CAGATTAAGGGCGCCAGCAGCCTTAGAGACTCCGGGCTCTTAAGCTTGTACTGCCAGTAGAGACT	360
OY	610	GTAAGCACTCAAACTTGGTACTTCATGTGTGAATGTGCACAGATGCCATCTCATCCGAGAT	669
Db	361	GTAAGCACTCAAACTTGGTACTTCATGTGTGAATGTGCACAGATGCCATCTCATCCGAGAT	420
OY	670	GATAGAGTGCACCCGATGGTGGGGAAGATTTGTCAAGTAGAACAGTAACAAAGA	729
Db	421	GATAGAGTGCACCCGATGGTGGGGAAGATTTGTCAAGTAGAACAGTAACAAAGA	480
OY	730	GCACCATACTTGGACACACAGAAAAGATGAAAAGCGGCTCATAGTGCCTTGCAGCC	789
Db	481	GCACCATACTTGGACACACAGAAAAGATGAAAAGCGGCTCATAGTGCCTTGCAGCC	540
OY	790	AACACTGTCAAATTCCGCTCCAGCCCGGGGGAAACCCAAATGCCAAGCATCGGTGGCTG	849
Db	541	AACACTGTCAAATTCCGCTCCAGCCCGGGGGAAACCCAAATGCCAAGCATCGGTGGCTG	600
OY	850	AAAAACGGGAAGGATTAAAGCAGAGACATCGATTGGAGGCTACAAAGGTACGAACACAG	909
Db	601	AAAAACGGGAAGGATTAAAGCAGAGACATCGATTGGAGGCTACAAAGGTACGAACACAG	660
OY	910	CAGTGGAGCCCTAATTATGGAAGGTGTGGTCCCATCTGCAGAAAGGAATTAATACGTGTG	969
Db	661	CAGTGGAGCCCTAATTATGGAAGGTGTGGTCCCATCTGCAGAAAGGAATTAATACGTGTG	720
OY	970	GTCGAGAATGAATACGGGCTCATCATACACAGTACACCTTGATGTTGTGAGCAGATCG	1029
Db	721	GTCGAGAATGAATACGGGCTCATCATACACAGTACACCTTGATGTTGTGAGCAGATCG	780
OY	1030	CCTACCGGGCCATCTCTCCAAAGCGGAGCTGGGGCAAAATGSCCTCAAGTGGTGGAGAGA	1089
Db	781	CCTACCGGGCCATCTCTCCAAAGCGGAGCTGGGGCAAAATGSCCTCAAGTGGTGGAGAGA	840
OY	1090	GACGTAGATTGTCTGCTCAAGGTTTACAGTGAAGCCACGCCACATCCAGTGAATCAAG	1149
Db	841	GACGTAGATTGTCTGCTCAAGGTTTACAGTGAAGCCACGCCACATCCAGTGAATCAAG	900
OY	1150	CACGTGAAAAAGACGGCAGTAATATACGGGGCCGAGGGGCTCCCTACCTCAAGGTTCTC	1209
Db	901	CACGTGAAAAAGACGGCAGTAATATACGGGGCCGAGGGGCTCCCTACCTCAAGGTTCTC	960
OY	1210	AAGCGCGCGGTGTTAACACACCGAGCAAAAGATTGAGGTTCTCTAATTTGGAAATGA	1269
Db	961	AAGCACTCGGGGATAAATAGTTCCTCAATGCAAGAAAGTCTGGCTCTGT-----TCATATG	1014
OY	1270	ACTTTTGGAGACGCTGGGGAATATACGTGGTGGCGGTAATTCTATTTCAGATATCTTT	1329
Db	1015	ACCGAGGCGGATCGCGGGGAATATATATGTAGGTCTCCAAATTAATATAGGAGCGCCAAC	1074
OY	1330	CACCTCGCATGTGGACAGTTCTGGC-----AGCGCTGGAAGAGAAAAAGAGATT	1380
Db	1075	CAGTCTGCTCGCTCAGCTGTCTGCTCCAAAACAGCAAGCGCGCTGGAAGAGAAAGAGATT	1134
OY	1381	ACAGGTTCCCAAGACTACCTTGGAGATATAGCCATTACTGCATAGGGGTCTTCTTAATGCC	1440
Db	1135	ACAGGTTCCCAAGACTACCTTGGAGATATAGCCATTACTGCATAGGGGTCTTCTTAATGCC	1194
OY	1441	TGTATGGTGAACAGTATCTGTGGCGAATGAACACAGCAAGCAAGAACGACACATTC	1500
Db	1195	TGTATGGTGAACAGTATCTGTGGCGAATGAACACAGCAAGCAAGAACGACACATTC	1254
OY	1501	AGCACCCAGCCGGCTGTGCACAACTTACCAAAAGTATCCCCCTGGGAGACAGGTACA	1560

[illegible]

```

US-08-471-570-5
; Sequence 5, Application US/08471570
; Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: IGARASHI, Koichi
APPLICANT: SENOO, Masaharu
APPLICANT: MATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:
APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINER, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO.: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..1953
US-08-471-570-5

Query Match          42.6%; Score 1817.2; DB 1; Length 1954;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 58; Indels 15; Gaps 2

OY 250 GGACCGGGGATGTGATCCGTAACCATATGCATCTGGAGTGTCTTCATCGCCGTGGCGTG 309
      |||
Db   1 GGACCGGGGATTTGATCGTATACCATATGCATCTGGAGTGTCTTCATCTGCCGTGGCGTG 60

OY 310 GTACCACTATGCACAACCTTGTCTCCCTGGCCGGCCCTCTTCATGTTTAGTTAGAGTATACACA 369
      |||
Db   61 GTACCACTATGCACAACCTTGTCTCCCTGGCCGGCCCTCTTCATGTTTAGTTAGAGTATACACA 120

OY 370 TTAGAGCCAGAAGACGACCAACCAAAATTCGAATCTCTCAACGACGAATGTACGTGGCT 429
      |||
Db   121 TTAGAGCCAGAAGACGACCAACCAAAATTCGAATCTCTCAACGACGAATGTACGTGGCT 180

OY 430 GCGCCAGGAGATCGCTAGAGGTGCGCTGCTGTTGAAAGATGCGCCGCTGATCAGTTGG 489
      |||
Db   181 GCGCCAGGAGATCGCTAGAGGTGCGCTGCTGTTGAAAGATGCGCCGCTGATCAGTTGG 240

OY 490 ACTAAGATGGGGTCACTTGGGGCCCAACAATAGAGACAGTCTTATTGGGAGTACTTGG 549
      |||

```

Db	241	ACTAAGGATGGGGTGCACCTTGGGGCCCAACAATAGCACTGCTTATTTGGGGAGTACTTG	300
Qy	550	CAGATTAAGGGGGCGCCAGCCCTAGAGACTCCGGGCTCATGCTTGTACTCCAGTAGACT	609
Db	301	CAGATTAAGGGGGCGCCAGCCCTAGAGACTCCGGGCTCATGCTTGTACTCCAGTAGACT	360
Qy	610	GTAGCACTGAAACTGGTACTTCATGTTGAATATGCACAGATGCCATCTCATCCGGAGAT	669
Db	361	GTAGCACTGAAACTGGTACTTCATGTTGAATATGCACAGATGCCATCTCATCCGGAGAT	420
Qy	670	GATGAGATGACACCGAATGTTGGGGGAATTTTGTCAGTGAAACAGTAAACAAGAGA	729
Db	421	GATGAGGATGACACCGAATGTTGGGGGAATTTTGTCAGTGAAACAGTAAACAAGAGA	480
Qy	730	GCACCATCTGTGACCAACACAGAAATATGAAAGAGGGCTCCATGCTGTGGCTGGGCC	789
Db	481	GCACCATCTGTGACCAACACAGAAATATGAAAGAGGGCTCCATGCTGTGGCTGGGCC	540
Qy	790	AAACATGTCAGATTTCGTGCGTCCGACGGGGGGGAACCCATATGCCAATGCGGTGGTG	849
Db	541	AAACATGTCAGATTTCGTGCGTCCGACGGGGGGGAACCCATATGCGGTGGTG	600
Qy	850	AAAAACGGGAAGGATTTAAGCAGAGACATGCAATTGAGAGCTTACAAGGTACGAACACAG	909
Db	601	AAAAACGGGAAGGATTTAAGCAGAGACATGCAATTGAGAGCTTACAAGGTACGAACACAG	660
Qy	910	CACGTGACCTCATTTATGGAAGGTGTGTCCCATGTGACAAAGGAATTAATACGTGTG	969
Db	661	CACGTGACCTCATTTATGGAAGGTGTGTCCCATGTGACAAAGGAATTAATACGTGTG	720
Qy	970	GTGAGAAATGAATACGGGTCCATCAATACACGTACCACCTGGATTTGTGAGAGATG	1029
Db	721	GTGAGAAATGAATACGGGTCCATCAATACACGTACCACCTGGATTTGTGAGAGATG	780
Qy	1030	CCTACACGGCCCATCTCTCCAAAGCCGGGACCTCGGCAATATGCTTCCACAGTGTGGAGGA	1089
Db	781	CCTACACGGCCCATCTCTCCAAAGCCGGGACCTCGGCAATATGCTTCCACAGTGTGGAGGA	840
Qy	1090	GACGTAGATTGTCTCGAAGGTTTACAGTAGATGCCAGCCCAACATGCAAGTGATCAAG	1149
Db	841	GACGTAGATTGTCTCGAAGGTTTACAGTAGATGCCAGCCCAACATGCAAGTGATCAAG	900
Qy	1150	CACGTGAAAAAGACGGCAGTAAATACGGGCCCGAGGGGCTGCCCTTCACTCAAGTTCTC	1209
Db	901	CACGTGAAAAAGACGGCAGTAAATACGGGCCCGAGGGGCTGCCCTTCACTCAAGTTCTC	960
Qy	1210	AAGCGCCCGGTGTTAAACACACCGGACAAAGACATTGAGTTCTCTATATTCGAATGTA	1269
Db	961	AAGCGCTCGGGATTAATAGTTCCAAATGCAAGAGTCTGTGCTCTGTTCTC-----AATGTG	1014
Qy	1270	ACTTTTGAGGACGGTGGGGAAATACGTGTTGGCGGTAATCTTATTTGGATATCTTT	1329
Db	1015	ACCGAGCGGATGCGGGGGAATATATATGTAAAGTCTCCAAATTAATATAGGCAAGCCAAAC	1074
Qy	1330	CACCTGCGATGTTGACAGATTTCGC-----AGCGCTTGAAGAGAAAAAGAGATT	1389
Db	1075	CAGTCTGCTGTGCTCACGTCTCTGCCAAAACAGCAAGCCGTGTGAAGAGAAAAAGAGATT	1134
Qy	1381	ACAGCTTCCCAAGACTACCTGAGAGATAGCCATTTACTCATAGGGGTCTTCTTAATCGCC	1440
Db	1135	ACAGCTTCCCAAGACTACCTGAGAGATAGCCATTTACTCATAGGGGTCTTCTTAATCGCC	1199
Qy	1441	TGTATGGTGTAAACAGTACATCTGTGCCGAATTAACAACACGACCAAGAAAGCCACATTC	1500
Db	1195	TGTATGGTGTAAACAGTACATCTGTGCCGAATTAACAACACGACCAAGAAAGCCACATTC	1254
Qy	1501	AGCAGCCAGCCGCTGTGTCACAAAGCTGACCAAAAGTATCCCTCGGAGAGAGGTAAACA	1560
Db	1255	AGCAGCCAGCCGCTGTGTCACAAAGCTGACCAAAAGTATCCCTCGGAGAGAGGTAAACA	1314
Qy	1561	GTTTGGGCTGAGTCCAGCTCTCTCCATGAACTCCAAACCCCGCTGTGTAGATTAACAACA	1620
Db	1315	GTTTGGGCTGAGTCCAGCTCTCTCCATGAACTCCAAACCCCGCTGTGTAGATTAACAACA	1374

QY 1621 CGCCTGCTTCAACGAGACACCCCATGCTGGAGGGGTCGAGTATGAACCTTCCA 1680
 Db 1375 CGCCTGCTTCAACGAGACACCCCATGCTGGAGGGGTCGAGTATGAACCTTCCA 1434
 QY 1681 GAGGACCCAAATGGAGCTTCCAGAGATAGCTGACACTGGGCAAGCCCTGGAGAA 1740
 Db 1435 GAGGACCCAAATGGAGCTTCCAGAGATAGCTGACACTGGGCAAGCCCTGGAGAA 1494
 QY 1741 GCTTCTTTGGGCAACTGCTCATGCGGAAAGCAGTGGGAATTGACAAAGCAAGCCCAAG 1800
 Db 1495 GCTTCTTTGGGCAACTGCTCATGCGGAAAGCAGTGGGAATTGACAAAGCAAGCCCAAG 1554
 QY 1801 GAGCGGTCACGCTGGCCGGAAGATGTTGAAGATGATGCCACAGAAAGACCTTCTC 1860
 Db 1555 GAGCGGTCACGCTGGCCGGAAGATGTTGAAGATGATGCCACAGAAAGACCTTCTC 1614
 QY 1861 GATCTGCTCAGAGATGAGATGATGAAGATGATGGGAACACAAAGATATCATTAAT 1920
 Db 1615 GATCTGCTCAGAGATGAGATGATGAAGATGATGGGAACACAAAGATATCATTAAT 1674
 QY 1921 CTCTTGGAGCTTCGACACAGATGGGCTCTTATGTCATGCTGATGCTCTTAA 1980
 Db 1675 CTCTTGGAGCTTCGACACAGATGGGCTCTTATGTCATGCTGATGCTCTTAA 1734
 QY 1981 GCGACCTCCGAGATACCTCCGAGCCGAGGCGACCCGGATGGAGTACTGCTATGAC 2040
 Db 1735 GCGACCTCCGAGATACCTCCGAGCCGAGGCGACCCGGATGGAGTACTGCTATGAC 1794
 QY 2041 ATTACCGTCTCTGAGAGAGATGACCTTCAAGACTTGGTGTGTCATGCACTACAG 2100
 Db 1795 ATTACCGTCTCTGAGAGAGATGACCTTCAAGACTTGGTGTGTCATGCACTACAG 1854
 QY 2101 CTGCGCAGAGCGATGAGTACTTGGCTTCCCAAAATGATTTGATGAGATTTAGAGCC 2160
 Db 1855 CTGCGCAGAGCGATGAGTACTTGGCTTCCCAAAATGATTTGATGAGATTTAGAGCC 1914
 QY 2161 AGAATGTTTGTGTAACAGAAACAAATGATGAATAAT 2200
 Db 1915 AGAATGTTTGTGTAACAGAAACAAATGATGAATAAT 1954
 RESULT 5
 US-08-471-570-9
 : Sequence 9, Application US/08471570
 : Patent No. 5750371
 : GENERAL INFORMATION:
 : APPLICANT: IGARASHI, Koichi
 : APPLICANT: SENOO, Masaharu
 : APPLICANT: MATANABE, Tatsuya
 : TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 : ADDRESSEE: CUSHMAN
 : STREET: 130 Water Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: US
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-471,570
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/149,664
 : FILING DATE:
 : APPLICATION NUMBER: US 07/743369

FILING DATE: 16-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 : NAME: LINER, Ernest V
 : REGISTRATION NUMBER: 29822
 : REFERENCE/DOCKET NUMBER: 40897
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617)523-3400
 : TELEFAX: (617)523-6440
 : TELEX: 200291 STRE UR
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2310 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 25..1980
 : US-08-471-570-9

Query Match 39.7%; Score 1692.8; DB 1; Length 2310;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 1778; Conservative 0; Mismatches 57; Indels 21; Gaps 3;

QY 728 GAGCACCATAGTGGACCAACAGAAAGATGAAAGGGGTCATGCTGGCTGGG 787
 Db 134 GAGCACCATAGTGGACCAACAGAAAGATGAAAGGGGTCATGCTGGCTGGG 193
 QY 788 CCAACACTGTCAGATTTCCTGCCAGCCGGGGGAACCCATGCCACATGCGGTGGC 847
 Db 194 CCAACACTGTCAGATTTCCTGCCAGCCGGGGGAACCCATGCCACATGCGGTGGC 253
 QY 848 TGAAGAACCGGAAGAGTTTAAGCAGAGATCGCATTTGGAGGCTTCAAGATGCAAAAC 907
 Db 254 TGAAGAACCGGAAGAGTTTAAGCAGAGATCGCATTTGGAGGCTTCAAGATGCAAAAC 313
 QY 908 AGCAGTGAAGCCATCATTAAGAAAGTGTGCTCCATCTGACAAGGGAATTTATCTGTG 967
 Db 314 AGCAGTGAAGCCATCATTAAGAAAGTGTGCTCCATCTGACAAGGGAATTTATCTGTG 373
 QY 968 TGGTGAAGATGAATAGGGTCCATCATCAGATGACAGTGGTGTGGAGCAT 1027
 Db 374 TGGTGAAGATGAATAGGGTCCATCATCAGATGACAGTGGTGTGGAGCAT 433
 QY 1028 CGCCTACCGGCCCATCTCCAAAGCCGAGCTGCCGGAATGCTTCACAGTGGTGGAG 1087
 Db 434 CGCCTACCGGCCCATCTCCAAAGCCGAGCTGCCGGAATGCTTCACAGTGGTGGAG 493
 QY 1088 GAGAGCTAGAGTTTCTCTCAAGGTTTACAGTATGCCAGCCGCAATCCAGTGAATCA 1147
 Db 494 GAGAGCTAGAGTTTCTCTCAAGGTTTACAGTATGCCAGCCGCAATCCAGTGAATCA 553
 QY 1148 AGCAGCTGGAAGAAAGACGAGTAAATACGGGCGCAGCGGCTGCCCTCACTCAAGGTT 1207
 Db 554 AGCAGCTGGAAGAAAGACGAGTAAATACGGGCGCAGCGGCTGCCCTCACTCAAGGTT 613
 QY 1208 TCAAGCCCGCGGTGTTAAACACCGAGACAAGAGATTAGGTTCTCTATTTCGAGATG 1267
 Db 614 TCAAGCCCGCGGTGTTAAACACCGAGACAAGAGATTAGGTTCTCTATTTCGAGATG 667
 QY 1268 TAACTTTTGAAGCGCTGGGGAATATACGCTTGGCGGGTATATGATGGATATCTCT 1327
 Db 668 TGAAGCGAGGCGATGCTGGGGAATATATATGATGGATATATGATGGGAGCGGCA 727
 QY 1328 TTCATCTGTCATGTTGACAGTCTGCC-----AGCGCTGGAAGAGAAAGAGACA 1378
 Db 728 ACCAGTCTGCTGCTGCTCAGCTGCTCTCCAAACAGCAACGCGCTGGAAGAGAAAGAGACA 787
 QY 1379 TTACAGCTTCCCGACAGTACCTGAGATAGCCATTTACTGATAGGAGGCTCTTAAATCG 1438
 Db 788 TTACAGCTTCCCGACAGTACCTGAGATAGCCATTTACTGATAGGAGGCTCTTAAATCG 847

QY 1439 CCTGTATGGTGTAAAGTCATCTGTGTCCGATGAAGAACACAGACCAGACAGACT 1498
 DB 848 CCTGTATGGTGTAAAGTCATCTGTGTCCGATGAAGAACACAGACCAGACAGACT 907
 QY 1499 TCAGCAGCCAGCCGCGTGTGCAACAACTGACCAACAGTATCCCTGCGGAGACAGTAA 1558
 DB 908 TCAGCAGCCAGCCGCGTGTGCAACAACTGACCAACAGTATCCCTGCGGAGACAG--- 963
 QY 1559 CAGTTTCGGCTGAGTCCAGCTCCCTCCATGAACTCAACACCCCGCTGTGTAGATTAACA 1618
 DB 964 --GTTTCGGCTGAGTCCAGCTCCCTCCATGAACTCAACACCCCGCTGTGTAGATTAACA 1021
 QY 1619 CACGCTCTCTTACAGCAGACACCCCAAGCTGCGAGGGGTCTCCGATGAACCTTC 1678
 DB 1022 CAGGCTCTCTTACAGCAGACACCCCAAGCTGCGAGGGGTCTCCGATGAACCTTC 1081
 QY 1679 CAGAGACCCAAATGGAGTTTCCAAGATTAAGTGAACACTGAGGGCAAGCCCTTGGAG 1738
 DB 1082 CAGAGACCCAAATGGAGTTTCCAAGATTAAGTGAACACTGAGGGCAAGCCCTTGGAG 1141
 QY 1739 AAGGTTGCTTTGGGCAAGTGTCTATGGCGAAGCAGTGGGAATTGACAAAGACGCCA 1798
 DB 1142 AAGGTTGCTTTGGGCAAGTGTCTATGGCGAAGCAGTGGGAATTGACAAAGACGCCA 1201
 QY 1799 AGGAGCGGCTCACCGTGGCGGTGAAGATGTTGAAGATGATGCCAGAGAAAGACCTTT 1858
 DB 1202 AGGAGCGGCTCACCGTGGCGGTGAAGATGTTGAAGATGATGCCAGAGAAAGACCTTT 1261
 QY 1859 CTGATCTGGTGTACAGATGAGATGATGAAGTGTGGAAACCAAGAAATATATA 1918
 DB 1262 CTGATCTGGTGTACAGATGAGATGATGAAGTGTGGAAACCAAGAAATATATA 1321
 QY 1919 ATCTTCTGGAGCCTGCACACAGATGGGCTCTCTATGTCAATAGTTGATGCTCTA 1978
 DB 1322 ATCTTCTGGAGCCTGCACACAGATGGGCTCTCTATGTCAATAGTTGATGCTCTA 1381
 QY 1979 AAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGGCCACCCGGAGTGAAGTCTTATG 2038
 DB 1382 AAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGGCCACCCGGAGTGAAGTCTTATG 1441
 QY 2039 ACATTAAACGCTTCTCTGAGAGACAGATGACCTTCAAGGCTGGTGTATGACCTACC 2098
 DB 1442 ACATTAAACGCTTCTCTGAGAGACAGATGACCTTCAAGGCTGGTGTATGACCTACC 1501
 QY 2099 AGCTGGCCAGAGCAGATGAGTACTTGGCTTCCCAAAATGTATTCATCGAGATTAGAC 2158
 DB 1502 AGCTGGCCAGAGCAGATGAGTACTTGGCTTCCCAAAATGTATTCATCGAGATTAGAC 1561
 QY 2159 CCAGAAATGTTTGGTAAACAGAAACAAATGTGTGAAATAGCAGACTTGGACCTGCCA 2218
 DB 1562 CCAGAAATGTTTGGTAAACAGAAACAAATGTGTGAAATAGCAGACTTGGACCTGCCA 1621
 QY 2219 GAGATATCAACAATATAGACTATTACAAAAGACCAACATGGGCGGCTTCCAGTCAAGT 2278
 DB 1622 GAGATATCAACAATATAGACTATTACAAAAGACCAACATGGGCGGCTTCCAGTCAAGT 1681
 QY 2279 GGAATGCTCCAGAAAGCCCTGTTGATAGATATACACTCATGAGTGTGCTGTCTCT 2338
 DB 1682 GGAATGCTCCAGAAAGCCCTGTTGATAGATATACACTCATGAGTGTGCTGTCTCT 1741
 QY 2339 TCGGGGTGTTAATGTGGGATCTTCACTTAGGGGGCTGCGCTTACCCAGGAGATTCCCG 2398
 DB 1742 TCGGGGTGTTAATGTGGGATCTTCACTTAGGGGGCTGCGCTTACCCAGGAGATTCCCG 1801
 QY 2399 TCGAGAACTTTTAAAGTGTGAAGAGACACAGATGATTAAGCCAGCAATGCA 2458
 DB 1802 TCGAGAACTTTTAAAGTGTGAAGAGACACAGATGATTAAGCCAGCAATGCA 1861
 QY 2459 CCAAGAACTGTACATGATGATGAGGAGCTGTTGGCATGACCTGCCCTCCAGAGACCAA 2518
 DB 1862 CCAAGAACTGTACATGATGATGAGGAGCTGTTGGCATGACCTGCCCTCCAGAGACCAA 1921
 QY 2519 CGTCAAGAGCTTGGTGAAGAGACTTGGATGCAATCTCCTCACACCAACCAATGAG 2574

DB 1922 CGTTCAGCAGCTTGTGTAAGAACTGGATGCAATCTCACTCTCACACCAATGAG 1977
 RESULT 6
 US-08-070-165F-5
 ; Sequence 5, Application US/08070165F
 ; Patent No. 5750365
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiu, Ing-Ming
 ; APPLICANT: Poulin, Matthew L
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ing-Ming Chiu
 ; STREET: S2052 Davis Medical Research Center, 480 West
 ; STREET: 9th Avenue
 ; CITY: Columbus
 ; STATE: Ohio
 ; COUNTRY: USA
 ; ZIP: 43210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/070,165F
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (614)-293-8093
 ; TELEFAX: (614)-293-5631
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2675 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: No. 5750365ophthalmus viridescens
 ; DEVELOPMENTAL STAGE: Adult
 ; TISSUE TYPE: Regenerating forelimb blastema
 ; CELL TYPE: Mesenchyme and Epithelium
 ; IMMEDIATE SOURCE:
 ; LIBRARY: lambda gt11
 ; CLONE: KP23-1
 ; POSITION IN GENOME:
 ; UNITS: bp
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..324
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 325..2511
 ; FEATURE:
 ; NAME/KEY: 3'UTR
 ; LOCATION: 2512..2675
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Poulin, Matthew L
 ; TITLE: Nucleotide sequences of two new
 ; TITLE: Factor Receptor-2 variants
 ; JOURNAL: Biochim. Biophys. Acta
 ; VOLUME: 1220
 ; PAGES: 209-211
 ; DATE: 1994
 ; RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 2675
 ; US-08-070-165F-5

Query Match	32.0%;	Score 1367.6;	DB 1;	Length 2675;
Best Local Similarity	79.1%;	Pred. No. 0;		
Matches 1654;	Conservative 0;	Mismatches 429;	Indels 9;	Gaps 2

QY	648	AGGGCCATCTTCATCGGGAGATGATAGAGTATACACCCGATGGTGGCGAAGATTTTGTGCAG	707
Db	432	AGATGCAAACTCATCAGGGATGATATACAGCAACAACGCGCTCGGAAGATTTTCACAA	491
QY	708	TGACAACTGTAAACACAAAGAGACACCACTACTGTGACCAACACAGAAAAAGATGTGAAAAAGCG	767
Db	492	TGACAAAC - - - AACACATGAGGGCTCCGTAACTGTGAGAGAAATACGAAAAATTGTGAAAAAGAA	548
QY	768	GCTTCATGCTGTGCTGTGCGGCCAAACACTGTCAAAGTTTGGCTGTGCCAGCCGGGGGGAACCC	827
Db	549	ACTTCATGCTGTGCTGCGCTGCCCAACCTGTGAAGTTTCCGCTGTCCAGCGCGGTGCACACCC	608
QY	828	AATGCGCAACACTCGGTCGCTGTAAGAAAGGAGAGTTTAAGCAGAGACATCGCATTTGG	887
Db	609	TAGCGCCCTCCATGATGATGTCGTGAAGAAAGCGCAAGAGATTCAAGCAGAGACACCCGATTTGG	668
QY	888	AGGCTACAGGTACGAAACCAACGACGCTGAGAGCTCATTTATGAGAAAGTGTGCCATCTGA	947
Db	669	CGGCTTCAAGGTACGTAGTCAACACTTCAAGCTGTATCAAGAGACGTCGTCTCCCTCTGA	728
QY	948	CAGAGGAAATTTATACCTGTGTGTGTGAGAAATGATATACGGTGTCCATCATCTACAGGTACCA	1007
Db	729	CGAGGGCAACTACACCTGTATCTATGAGAGAACGATGTGGATCTCATCATCAACACCTTACCA	788
QY	1008	CGTGGATGTTGTGTGAGAGATCGCCCTTCACCGCGCCATCTCCAAAGCGGAGATCGCGCAAA	1067
Db	789	CGTGGATGTTGTGTGAGAGGGTACACCCGACCGGCAATATCTCCAAAGCTGTGGGGCTTCGGGCAAA	848
QY	1068	TGCTCTCCACAGTGTGTGCGAGAGAGCTAAGAGTTTGTCTGCAAGGTTTACAGTATGCCCA	1127
Db	849	CACACACCAACAAAGTTGTGGGGGCGCATCAAGAGTTTGTGTTGTCGAAAGCTCTCAGAGTACGCA	908
QY	1128	GCGCCCATCATCAGTGGATCTCAAGACGTGTGAAAAAGAACGGCAGCTAAATACGGGCCGACAG	1187
Db	909	GCACATATCTCATATGATTTGTGACATTTTGTAGCTGAATGGCAATAAAAATTGGACCTGACGG	968
QY	1188	GCTGCGCTATCTCAAGGTTCTCAAGGCGCGCGGTGTTAAACACACGACCAAGAGATTTGA	1247
Db	969	GCATCCCTATCTGAAAGTGTCTAAAGCGCGCGGTGTTAAACACGAGCAAAAGATTTGA	1028
QY	1248	GGTTCCTATATTCGGAATGTAACTTTTGAAGACGCTGGGGAAATTTACGTGCTTGTGGCGGG	1307
Db	1029	AGTCTCTATATGTGGCAATGTCTCTTTTGAAGATGTGTGGGAGTATACGTGCTTGTGGCGGG	1088
QY	1308	TAAATTATTTGGGATATCTCTTTCACCTGCTCATGTGTGACAGTTCGTGCGACGCGCTGGAAG	1367
Db	1089	TAAATTATTTGGGATATCTCTTTCACCTGCTCATGTGTGACAGTTCGTGCGACGAGTGAAGAACG	1148
QY	1368	AGAAAAGAGATTTACAGCTTCCCAACATCACTGGAGATAGCCATTTACTGATAGGGGT	1427
Db	1149	GGAAGCTGGA - - - - - TTGATCATCTAGGAGATACGGAAGAAAGGCACTCTACTGTGTGGAGG	1202
QY	1428	CTTCTTAAATCGGCTGTATGTGTGTGTAAAGTCACTGCTGCTCCGAATGGAAGAACACAGACAAA	1487
Db	1203	CTTCTCTATCACTCGCATGTATGTGCAACATCATGTGTGTGCCACATGAAAGGACAGAGGCA	1282
QY	1488	GAAAGCAAGCTTACGACAGCCAGCGCGGTGTGCAAGAGTGTACCAAGATTCCTCCCTCGG	1547
Db	1263	GAAATCTGACTTACGACAGCCACCGCTGTGCAAGAGTGTGACAGAGAGTCTCCCTCGG	1322
QY	1548	GAGACAGGTAAAGTTTCCGGCTGAGTGCAGAGTCTCTGCATGAAGCTCCAACACCCCGCTGT	1607
Db	1323	CAGACAGGTAAAGTGTCTGTCTAGTCAAGCTCTTCTATGAAGCTCCAAACATCTCACTGT	1382
QY	1608	GAGATTAACAAACAGCCTCTCTTCAAGCGCAGACACCCCATGTGTGAGAGGGGTCTTCGA	1667
Db	1383	CGGATACACACATCTGCTGTCTTCCAAACATGACACCCCATCTGTGTGCGCGGGGTCTCCGA	1442
QY	1668	GTAATGAACTTCCAGAGAGCAACCAAAATGTGGAGTTTCCAAAGATTAAGCTGTACACTGGGCA	1727

Db	1443	GTATAGAGCTGCCAGAGAGACCCCAAGTGGGAGATATCCAAAGGAAAAAGCTCAGCGTGGGAA	1502
Qy	1728	GCCCTGGAGAGAGTCTTTGGGCAAGTGTCATGCGGGAAGCAGTGGGAATTGACAA	1787
Db	1503	GCCCTGGGCGAAGGCTGCTTCGGGCAGGTGTGATGTCAGAGGGGGGTGGGATGCACAA	1562
Qy	1788	AGACAGACCCCAAGAGGCGGTACCGTGGCGGTGAAGATGTTGAAAGATGATGCCACGA	1847
Db	1563	GGACGCGGCGCAAAAGATGAGAGCGCCGTGGCAGTGAAGATGCTGAAAGACGATGCCAACGA	1622
Qy	1848	GAAGACCTTCTGATCGTGGTGCAGAGATGAGATGATGAAAGATGGGAAACACAA	1907
Db	1623	CAGAGATCTTTCTGATCTGGTGTCTGAGATGAAATGATGAAGATGATTTGGAGACATAA	1682
Qy	1908	GAATATCATAAATCTTCTTGAAGCCCTGCACACAGAGATGGGCTCTATATGTATAGTTGA	1967
Db	1683	AAATATCATCATATCTTCTAGAGAGCTGCACCCAAAGATGGCCCACTCATGTGATAGTGA	1742
Qy	1968	GTAATCCCTTAAAGCAACCTCCAGAAATACCTCCGACCCGGAGGCCACCCGGATGGA	2027
Db	1743	ATATCCCTTCAAGGGGAACCTCGGAAATACTGCGCACCCGCCCCCACTGGGATGGA	1802
Qy	2028	GTACTCCATGATGATTAACCGGTCTCGAGAGAGAGATGACCTTCAAGGACTTGGTGTGC	2087
Db	1803	GTACTCCCTTGAACATCAACAGAAATTCCTGAAAGAGCAGATGACCTTCAAGGACCTTAGTGTG	1862
Qy	2088	ATGCACCTACAGCTGGCGCAGAGCGCATGAGTACTTGGCTTCCCAAAAATGATTCATCG	2147
Db	1863	TTGCACGTACCAACATCGGCGAGGGGAATGAGTACTGGGATCAGAAAGTGCATCCTCG	1922
Qy	2148	AGATTACAGCGCAAAATGTTTTGGTAAACAGAAAACAATGATGAAATAGCAGACTT	2207
Db	1923	GGACTTGGCAGTCCGAATGCTTGGTGAACGGAACCAACGTCATGAATAATTCAGAAATTT	1982
Qy	2208	TGGACTCGCAGAGATCAACAAATATAGATTAACAAAAGACCAACAATGGACGGCT	2267
Db	1983	TGGTTGGCGCCGAGCATTACACACATGACTACTACAAAAAACACCAATGGCGGCT	2042
Qy	2268	TCCAGTCAAGTGATGGCTCCAGAAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGA	2327
Db	2043	CCCCGTGAAGTGATGGCTCCCGAGGCGCTGTTTGACAGAGCTCACACATCAGAGTGA	2102
Qy	2328	TGTCTGTCTCTCGGGGTGTAAATGTGGAGATCTTTCACCTTAGGGGGCTGGCCTACCC	2387
Db	2103	CGTCTGGTCTTTCGGTGTGCTTATGTGGAGATCTTCCACACTGGGGGGGTCTCCCATACC	2162
Qy	2388	AGGGAATCCCGTGAGAGAACTTTTAAGCTGGTGAAGGAAGGACACAAATGGATTAAGCC	2447
Db	2163	TGGAATTTCCAGTTGAAGAATCTTTCAACTCTTTAAGGAAGGCCACCGAATGGACAAAGC	2222
Qy	2448	AGCCAATGTCACCAAGAACTGTATAGATGATGAGGAGCTGTGGCATGAGTGCCTTC	2507
Db	2223	TGGCAATGTCACCAATGAGCTGTATACAAATGATGACGAGACTCTGGCGGTGTGCCCTC	2282
Qy	2508	CCAGAGACCAAGCTTCAAGCAACTGTGTGAAGAACTTGAATGCAATTTCTACCTCAGAAC	2567
Db	2283	GCAAAGACCACTTTCAGCAACACTGTTGTGAGATGTAGACCGAAATCTTCACGCAAAACGAC	2342
Qy	2568	CAATGAGGAATCTTGAAGCACTCAGCAACCTCTCAACAGTATTTCAAGTATGATACCTTGA	2627
Db	2403	TACCAAGGATTCCTGCTCTTCTGGGAGTAGACTCTGCTTCTCCCGGACGCAATGCCCTA	2462
Qy	2688	CGAACCATGCTCTCTCAATATCCACACATAAAGGCGAGTGTAAACATGGA	2739
Db	2463	CGACCCCTGTCTCCCAATCCCAACACAAACGCGACACATTAATAACATGA	2514

RESULT 7

US-08-885-418-5
Sequence 5, Application US/08885418
Patent No. 5925528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Matthew L.
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 52052 Davis Medical Research Center, 480 West
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2675 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: No. 5925528ophthalmus viridescens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating forelimb blastema
CELL TYPE: Mesenchyme and Epithelium
IMMEDIATE SOURCE:
LIBRARY: lambda gt11
CLONE: KP23-1
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..324
FEATURE:
NAME/KEY: CDS
LOCATION: 325..2511
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 2512..2675
PUBLICATION INFORMATION:
AUTHORS: Poulin, Matthew L
TITLE: Nucleotide sequences of two new
TITLE: (No. 5925528ophthalmus viridescens) fibroblast growth
JOURNAL: Biochim. Biophys. Acta
VOLUME: 1220
PAGES: 209-211
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 2675
US-08-885-418-5
Query Match 32.0%; Score 1367.6; DB 2; Length 2675;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 1654; Conservative 0; Mismatches 429; Indels 9; Gaps 2;

Db 432 AGATGCAAACTCATCAGGGGATGATGAAGACGACAAAGCAGCGGTCGGAACATTTTCACAA 491
Oy 708 TGAGAACAGTAACAAAGAGAGACACATCTGACCAACAGAAAGATGAAAGCG 767
Db 492 TGACAAAC---ACCACATAGGGGCTCGTACTGAGACAAATACGAAATAATGGAAAGAA 548
Oy 768 GCTCATGCTGTGCTGCGCCGCAACACTGCAAGTTTCGCGCCAGCGGGGGAACCC 827
Db 549 ACTTCATGCTGTGCGCCGCTCCCAACTGTGAAGTTTCGCTGTCACGCGGTGCAACCC 608
Oy 828 AATGCCAACCATCGCGTGGTGAAGAAAGGGAAGAGTTTAAAGCAGAGCATGCAATTGG 887
Db 609 TACGCCCTCATGAGGGGTGGAAGAACGCAAGAGTTCAACAGAGACAGCCGCAATTGG 668
Oy 888 AGGCTACAGAGTACGAACACGACGACCTGATATTGAAAGTGTGCTCCATCTGA 947
Db 669 CGGCTTCAGAGTACGATGACACTTACACCTGATCATGAGACGCGTGGTCCCTCTGA 728
Oy 948 CAAGGCAAAATTATACCTGTGTGGGAGATGAATAGGGGTCCATCATACAGTACCA 1007
Db 729 CGAGGGCACTACACCTGTATCATGGAAGAGATGATTCATCATACATCACATACCA 788
Oy 1008 CCTGGATGTTGTGAGAGATCGCCTACCGGCCCATCTCCAAAGCGGACTGCGGCAAA 1067
Db 789 CTGTGATGTTGTGAGAGGTCACCCACCGGCCCAATCTCCAAAGTGGGCTTCCGGCAAA 848
Oy 1068 TGGCTCCACAGTGTGGGAGAGACGTAGAGTTGTCTGCAAGCTTTACAGTATGCCA 1127
Db 849 CACACCCACAAAGTTGGGGGCGATGAGAGTTGTTTGAAGTCAAGTACAGTACCCACA 908
Oy 1128 GCCCCACATCCAGTGGATCAAGCAGCGTGAAGAAAGAGCGGAGTAATACGGGCGGCA 1187
Db 909 GCCACATATCATGATGATTTGACATTTTGAAGCTGAATGCGAGTAATTTGACATGACG 968
Oy 1188 GCTGCCCTACCTCAAGTTCTCAAGCGCGCGCGTGTAAACCCACGACGACAAAGATTGA 1247
Db 969 GCATCCCTATCTGAAAGTGTAAAGCGCGCGGTGTAAACCCACGACGACAAAGATTGA 1028
Oy 1248 GGTTCCTAATTCGGAATGTAATCTTTGAGAGCGCTGGGGAATATACGTCTTGGCGGG 1307
Db 1029 AGTCCCTATGTCGGAATGTCCTTTTGGAGATGCTGGGAGATATACGTCTTGGCGGG 1088
Oy 1308 TAATTCATTTGGGATATCTCTTCACTCTGCATGATGATGACAGTCTGCGACCGCTGGAAG 1367
Db 1089 TAATTCACGGGATCTCTATACACTGATGATGATGATGATGATGATGATGATGATGAT 1148
Oy 1368 AGAAGAGAGATTACAGCTTCCAGAGTACCTGAGAGATTAGCATTTACTGCTAGAGCGT 1427
Db 1149 GGAAGTGA-----TTTCAATCATCGGAGATATACGGAATCGCATCTAGTGTGGGAGG 1202
Oy 1428 CTTCTTAATCGCCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1487
Db 1203 CTTCTGATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
Oy 1488 GAAGCCAGACTGACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1547
Db 1263 GAAGTGTGACTTGAAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1322
Oy 1548 GAGACAGGTAACGTTTGGCTGAGTTCAGCTCTCATGAACTCCAAAGACCCCGCTGGT 1607
Db 1323 CAGACAGGTAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382
Oy 1608 GAGGATACAAACAGCGCTCTCTTCAACGCGACAGACCCCATGCTGGCAGGGGTCTCCCA 1667
Db 1383 CCGGATACCACTGCGCTGTCTTCAACAAATGACACCCACTTGGCGGGGTCTCCCA 1442
Oy 1668 GTATGAACCTTCAGAGACCCAAATGAGAGTTTCCAAAGATATACCTGAGCGGCA 1727
Db 1443 GTATGAGCTGCGAGAGACCCCAAGTGGGATATCCAAAGGAAAGCTACCTGGGGA 1502
Oy 1728 GCCCTGGGGAAGGTTGCTTTGGGCAAGTGTATGCGGGAAGAGTGGGAATTGACA 1787

QY 1088 GAGACGTAGAGTTTGTCTGCAAGTTTACAGTATGCCAGCCACATCGATGATCA 1147
DB 494 GAGAGCTAGAGTTTGTCTGCAAGTTTACAGTATGCCAGCCACATCGATGATCA 553
QY 1148 AGCAGCTGAAAAAGAACGGCAGCTAAATACGGGCGCCAGCGGCTGCCATCTCAAGTTTC 1207
DB 554 AGCAGCTGAAAAAGAACGGCAGCTAAATACGGGCGCCAGCGGCTGCCATCTCAAGTTTC 613
QY 1208 TCAAGCGCGCGGCTGTAAACACCGAGCAAGAGATGAGTTCTCTATATTCGGAATG 1267
DB 614 TCACACACTCGGGGATTAATATCTTCCATGCAAGAGTGTGCTGTGT-----TCAAG 667
QY 1268 TAACTTTTGAAGACCGCTGGGAAATATACCTGCTGGCGGATCTTATTTGGGATATCT 1327
DB 668 TGACCGAGGCGGATCTGTGGGAAATATATATGTAAGTCTCCAAATATATAGGCGAGGCCA 727
QY 1338 TTCACTGTGATGTTGTAACAGTTTGC-----AGCGCTGGAAGAGAAAGAGA 1378
DB 728 ACCAGCTGTGCGCTGCTACCTGCTCCAAACACCAAGCGCTGGAAGAGAAAGAGA 787
QY 1379 TTACAGCTTCCCGACAGTACCGGAGATAGCCATTACGTGCTAGGGCTCTTAATCG 1438
DB 788 TTACAGCTTCCCGACAGTACCGGAGATAGCCATTACGTGCTAGGGCTCTTAATCG 847
QY 1439 CCTGTATGTTGTTAAACAGTATCTGTGCGGAATGAGAACAGACCAAGAGCCAGACT 1498
DB 848 CCTGTATGTTGTTAAACAGTATCTGTGCGGAATGAGAACAGACCAAGAGCCAGACT 907
QY 1499 TCAGAGCAGCAGCGGCTGTGCCAAGCTGACCAACGATATCCCTCGGAGACAGTTAA 1558
DB 908 TCAGAGCAGCAGCGGCTGTGCCAAGCTGACCAACGATATCCCTCGGAGACAGTTAA 963
QY 1559 CAGTTTGGCTGAGTCCAGCTCTCCATGAATCCACACCCCGTGGTGAAGATTAACAA 1618
DB 964 --GTTTGGCTGAGTCCAGCTCTCCATGAATCCACACCCCGTGGTGAAGATTAACAA 1021
QY 1619 CAGCGCTCTTTCAACGGCAGACACCCCATGCTGCGAGGGGTCTCCGATGTAAGTTTC 1678
DB 1022 CAGCGCTCTTTCAACGGCAGACACCCCATGCTGCGAGGGGTCTCCGATGTAAGTTTC 1081
QY 1679 CAGAGGACCCAAATGSGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAG 1738
DB 1082 CAGAGGACCCAAATGSGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAG 1141
QY 1739 AAGTTTGGTGGGCAATGATGATGGGGAAGCAGTGGGAATTACAAAGCAAGCCCA 1798
DB 1142 AAGTTTGGTGGGCAATGATGATGGGGAAGCAGTGGGAATTACAAAGCAAGCCCA 1201
QY 1799 AGAGGCGGCTACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACTTT 1858
DB 1202 AGAGGCGGCTACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACTTT 1261
QY 1859 CTGATCTGTGTCAAGATGATGATGAAGATGATGGCAACACAGAATATCATTA 1918
DB 1262 CTGATCTGTGTCAAGATGATGATGAAGATGATGGCAACACAGAATATCATTA 1321
QY 1919 ATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCTAGTTGATGCTGCTCA 1978
DB 1322 ATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCTAGTTGATGCTGCTCA 1381
QY 1979 AAGGCAACCTCCGAGAAATACCTCCAGCCCGGAGCCACCCGGATGAGTACTCTATG 2038
DB 1382 AAGGCAACCTCCGAGAAATACCTCCAGCCCGGAGCCACCCGGATGAGTACTCTATG 1441
QY 2039 ACATTAAACCGTGTCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2098
DB 1442 ACATTAAACCGTGTCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1501
QY 2099 AGCTGCGCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2158
DB 1502 AGCTGCGCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1561

QY 2159 CCAGAAATGTTTGGTAAACAGAAACAAATGATGATAAATAG 2200
DB 1562 CCAGAAATGTTTGGTAAACAGAAACAAATGATGATAAATAG 1603

RESULT 9
US-08-070-165F-9
Sequence 9, Application US/08070165F
Patent No. 5750365

GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (afgf)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Ing-Ming Chiu
STREET: 52052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2681 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: No. 5750365ophthalmus viridescens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating forelimb blastema
CELL TYPE: Mesenchyme and Epithelium
IMMEDIATE SOURCE:
LIBRARY: lambda gt11
CLONE: Kp19-1
POSITION IN GENOME:
UNITS: bp

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..324
FEATURE:
NAME/KEY: CDS
LOCATION: 325..2517
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 2518..2681
PUBLICATION INFORMATION:
AUTHORS: Poulin, Matthew L
TITLES: Nucleotide sequences of two newt
TITLES: (No. 5750365ophthalmus viridescens) fibroblast growth
JOURNAL: Biochim. Biophys. Acta
VOLUME: 1220
PAGES: 209-211
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 9: FROM 1 TO 2681

US-08-070-165F-9

Query Match 29.9% Score 1276.4; DB 1: Length 2681;
Best Local Similarity 76.6% Pred. No. 8.6e-304;
Matches 1607; Conservative 0; Mismatches 476; Indels 15; Gaps 3;

Qy 648 AGATGCATCTCATCCGAGATGATGAGATGACACCGATGGTGGGAAGATTTGTGAG 707
Db 432 AGATCAAACTCATCAGGAGATGATGAAGACACAAACGCGCTCGAAGATTTGACAAA 491
Qy 708 TGAGAACACTAACACAGAGAGCACCCTACTGACACCAACAGAGAAAAGATGAAAAGC 767
Db 432 TGACAAAC---AACCAAGATGAGGGCTCCGTACTGCGAATACGAAAAATTTGGAAAAA 548
Qy 768 GCTCATGCTGTGCTGGGGCCCAACACTGTCAAGTTTGGCTCCGACGGGGGGGAAACC 827
Db 549 ACTCATGCTGTGCGCCGCTGCCAACACTGTGAAAGTTCCGCTCTCAAGCCGGTGGCAACC 608
Qy 828 AATGCCAACCATGCGGTGGCTGAAAAACGGGAAGATTTTAAAGAGAGCATGCGATTGG 887
Db 609 TACGCCCTGCATGAGGTGGCTGAAGACGGCAAGATTCAAGAGAGACACGCGATTGG 668
Qy 888 AGGCTACAGAGTACGAAACACGACACTGAGCCTCATTTAGAAATGTGTGCCATCTGA 947
Db 669 CGGCTTCAAGAGTACTACTCAACACTTACGCTGATGAGAGCGTGTCCCTCTGA 728
Qy 948 CAAGGCAATTTATACCTGTGTGTGAGATGATACGGGTCCATCATACACAGCTACCA 1007
Db 729 CGAGGGCACTACACCTGTATCATGAGAACAGCATGATGATCCATCATACACACTTACCA 788
Qy 1008 CCTGATGTTGTGAGCAGCATGCGCTACCGGCCCATCTCCAAAGCGGAGATGCGGCAAA 1067
Db 789 CCTGATGTTGTGAGCGGCTACCGGCCCATCTCCAAAGCGGAGATGCGGCAAA 848
Qy 1068 TGCCCTCCACAGTGTGTGAGAGAGAGTGTGTCTGCAAGTTTACAGTATGCCCA 1127
Db 849 CACAACACCAAAAGTTGGGGGAGATGACAGAGTTTGTGCAAAAGCTACAGAGACCA 908
Qy 1128 GCGCCACATCCAGTGGATCAACAGCATGTAAGAAAGAGAGCATTAATAGGGCCGAGCG 1187
Db 909 GCGACATATCCATGATGATTTCCGATTTTGAAGTGAATGAGCAATAATTTGACCTGACG 968
Qy 1188 GCTGCGCTACCTCAAGGTTCTCAAGGCGCGGTGTAACACACGAGCAAAAGATGGA 1247
Db 969 GCATCCCTATCTGAAAGTGTCTAAAGCGCTCTGGAATTAATAGCTC-----CAATGCCGA 1022
Qy 1248 GGTTCCTATATTCGAGATGTAACTTTGAGAGACGCTGGGGAATTAAGCTGTTGCCGG 1307
Db 1023 ACTTCTGACCTGCATCAACGTGACTGAGGCGGACCGGGCCAGTACATGCAAAAGTCTC 1082
Qy 1308 TAATTCTAATGGGATATCCTTTCACTCTGCATGATGTCAGAGTTCGCGAGCGCTGGAAG 1367
Db 1083 CAATTATATTTGGGAGGCGCAACCACTCTGCGCTCAAGGTGTCTGCTCATGAGAGA 1142
Qy 1368 -----AGAAAAGAGATTTAAGCTTCCCAAGACTACTGAGATAGCCATTTACTGAT 1421
Db 1143 AGATGAAGAACGGGAAGTGAATTCATCATCGAGATACGGAATAACGCCATCTACTGTGT 1202
Qy 1422 AGGGGTCTTTTAATCGGCTGTATGGTGTAAACATCATCCTGTCCGGAATGAAGAACAC 1481
Db 1203 GGGAGGCTTCTGATACCTGTGATGTTGGCAATCATGTGTGCCACATGAAGGAG 1262
Qy 1482 GACCAAGAACCCAGACTTCAGAGCGAGCGGCTGTGCAACAGTGTACCAAAAGCTATGCC 1541
Db 1263 AGCAAGAAAGTGTGACTTCAGAGCGCACCGCTGTGCAAAAGCTGTAGAGAGAGTCTGCC 1322
Qy 1542 CCTGGGAGAGAGTAAAGATTTGGCTGAGTCAAGCTCTCCATGAATCCCAACAGCC 1601
Db 1323 CCTGGGAGAGAGTAAAGAGTGTGTGACTCAAGCTCTTTTATGAAGTCAACAGCTCC 1382
Qy 1602 GCTGTGAGAGTAAACACAGCGCTCTTTCAAGGCGAGACACCCCATGTGTGGAGGGGT 1661
Db 1383 ACTGTGCGGATCAACCTGCTGTCTTCCAAACAAATGACACCCACTTGTGGCGGGGT 1442

Qy 1662 CTCCAGTATGAACTTCCAGAGAGACCCAAAATGGGAGTTTCCAAAGATTAAGCTGACACT 1721
Db 1443 CTCCAGTATGAGCTGCCAGAGAGACCCAAAGTGGAGATATCCAAAGGAAAAAGCTCACCT 1502
Qy 1722 GGGCAAGCCCCGAGAGAGTGTGCTTGGCAAGTGTCTATGGCGGAAGAGTGGAT 1781
Db 1503 GGGCAAGCCCCGAGAGAGTGTGCTTGGCGAGTGTGTATGAGAGGGGTGGGAT 1562
Qy 1782 TGACAAAGAACCCCAAGAGAGCGGCTCACCGTGGCCGTGAAGATGTTGAAGATGATGC 1841
Db 1563 CGACAAGAGCGGGCCAAAGATGACGAGCGTGGCACTGAAAGATGTGAAGAGATGC 1622
Qy 1842 CACAGAGAAAGACCTTTCTGATCTGTGTCAAGAGATGAGATGATGATGATGGGAA 1901
Db 1623 AAGCAGAAAGATCTTTCTGATCTGTGTGTGAGATGGAATGATGAAGATGATGGGAA 1682
Qy 1902 ACACAAGATATCATTAATCTTTGAGAGCTGCACACAGATGGGCTCTCTATGTAT 1961
Db 1683 GCATAAATATCATCATATCTTCTAGAGAGCTGCACCAAGATGGCCACTCTAGTGTAT 1742
Qy 1962 AGTTAGTATGCTCTTAAAGCAACCTCCGAGATATCTCCGAGCGCGGAGCCACCGG 2021
Db 1743 AGTCGAATATGCTTCCAAAGGGAAGTGTGGAATATCTTGGCACCCGCCCACTGG 1802
Qy 2022 GATGAGTACTCTTATGACATTAACGCTGTCTGAGAGAGCAGATGACCTTCAAGACTT 2081
Db 1803 CATGAGTATCTCTTGTGATCATACAGAAATCTCTGAAGAGAGATGACCTTCAAGACTT 1862
Qy 2082 GGTGTATGACACCTTACAGCTGGCCAGAGAGATGAGATACCTTGGCTTCCAAAATGTAT 2141
Db 1863 AGTGTCTGACAGTACCAATGTGGCCAGGGAATGAGTACCTGATCAAGAAATGTAT 1922
Qy 2142 TCATGAGATTTAGAGGCGAGAAATGTTTGTGTAACAGAAAAATGTGATGAATATGC 2201
Db 1923 CCATGGGAGCTTGGAGCTGCGAAATGCTGTGTGACGGAACCAACGTCATGAATAATGTC 1982
Qy 2202 AGACTTGGAGCTCGCCAGAGATATCAACATATATAGACTATTAACAAAAGACCAACATGG 2261
Db 1983 AGATTTTGGTTTGGCCGAGACATCAACACATGACACTACATCAAAAAACACCAATGG 2042
Qy 2262 GCGGCTTCCAGTCAAGTGGATGCTCCAGAAAGCCCTGTTTGAATAGATATACATCATCA 2321
Db 2043 CCGGCTCCCGTGAAGTGGATGGCTCCGAGGCGCTGTTTGAACAGACTCACACATCA 2102
Qy 2322 GAGTATGATGCTGCTCGGGGTGTAAATGAGAGATCTTCACTTAAGGGGCTCGCC 2381
Db 2103 GAGTATGCTGCTGCTTGTGGGTGTGAGTGTGAGAGATCTTCACTGAGGGGCTTCCC 2162
Qy 2382 CTACCAGGATTTCCCTGAGAGAACTTTTAACTGCTGAAGAGAGACACAGAAATGA 2441
Db 2163 ATACCTGGAATTCAGTTGAAGAACTTTTCAAGCTCTTAAGAAAGGCGACCGAAATGA 2222
Qy 2442 TAAGCAGCCCACTGACCAACGAAGTGTACATGATGAGAGAGCTTTGGCATGACGT 2501
Db 2223 CAAGCTTGGCAACTGCACCAATGACATGTATACATGATGAGAGAGCTCTGCTGCTGT 2282
Qy 2502 GCGCTCCAGAGACCAAGCTTCAAGCATGTGTAAAGACTTGTGCAATTTCTACACT 2561
Db 2283 GCGCTGCAAGAACCCACTTTCACACACTTGTGTAGATCTAGACCAATCTTACGCA 2342
Qy 2562 CACAACAAATGAGAAATCTTGGATGAGCCAACTCTGCAAGAGATATTAACATAGTTA 2621
Db 2343 AAGCAACAAATGAGAGTACCTGAGACTCAACACCTCTGAGAGAGTACTGCCGACGTA 2402
Qy 2622 CCGTGACACAAAGATCTTGTCTTTCAGAGAGATGTTCTGTTTTCAGAGACCCAT 2681
Db 2403 TCCGATACAGAGATCTCTGCTTGTGGGATAGCTGTCTCTCCCGAGCAAT 2462
Qy 2682 GCCTTACGACCATGCTTCTGATATCCACACATTAAGCGGAGTGTAAACACATGA 2739
Db 2463 GCGCTAGACCCCTGTCTTCCAAATCCCAACACCAAGGCGACATTTAAACATGA 2520

```

RESULT 10
US-08-885-418-9
Sequence 9, Application US/08885418
Patent No. 5925528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 52052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2681 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: No. 5925528ophtalmus viridescens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating forelimb blastema
CELL TYPE: Mesenchyme and Epithelium
IMMEDIATE SOURCE:
LIBRARY: lambda gt11
CLONE: KP19-1
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..324
FEATURE:
NAME/KEY: CDS
LOCATION: 325..2517
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 2518..2681
PUBLICATION INFORMATION:
AUTHORS: Poulin, Matthew L
TITLE: Nucleotide sequences of two new
TITLE: (No. 5925528ophtalmus viridescens) fibroblast growth
TITLE: factor receptor-2 variants
JOURNAL: Biochim. Biophys. Acta
VOLUME: 1220
PAGES: 209-211
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 9: FROM 1 TO 2681
US-08-885-418-9
Query Match 29.9%; Score 1276.4; DB 2; Length 2681;
Best Local Similarity 76.8%; Pred. No. 8.6e-304;

```

[illegible]


```

: COUNTRY: USA
: ZIP: 10036/2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,296
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7573-024
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2469 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: MOLECULE TYPE: DNA
: NAME/KEY: Coding Sequence
: LOCATION: 1...2466
: OTHER INFORMATION:
:
: US-08-459-296-1

```

Query Match 27.7% Score 1182.2 DB 1: Length 2469;

Best Local Similarity 71.1% Pred. No. 1.1e-280; Matches 1616; Conservative 0; Mismatches 633; Indels 24; Gaps 3;

```

QY 458 GCCTGTTGAAGATGCCGCCGTGATGATGAGTGAAGATGGGGTGCATCTGGGCGCCA 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 GCGTGGGGAGCATGTGACAGATCACTGCGCGGAGCGGGGTGCACTGGCGGAAA 226
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 ACATAGACAGTGTATTATGGGAGTACTTGAGATTAAGGGCGCCAGCCCTAGAGACT 577
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 GCACACGCCACCCCATCACAGCGAGAGGTGAGGTGCGAGACTCGTCCCGCAGACT 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 578 CCGGCGCTATGCTGTACTGCGCATGAGACTAGACAGTGAATCTGGTACTTCTATG 637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 CCGGCGCTATGCTGTACTGCGCATGAGACTAGACAGTGAATCTGGTACTTCTATG 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 TGAATGTCAGATGCCATCTCATCCGAGATGAGATGACACCGATGTCGCGAAG 697
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 TCATATGTTTCAGATGCTCTCCCTCTCGAGAGATGATGATGATGATGATGATGAT 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 698 ATTTTCTAGTGAACAGTACACAA-----GAGAGCAGCATACTGGA 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 407 CAGAGAGAGAAAGAAAGATTAACCAACCAACCAACCGTATGCCGTATGCTCATTTGGA 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 743 CCAACAGAGAAAGATGAGAAAGCGGCTCATGCTGTGCTGGGCGCAACCTGTCAAGT 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 467 CATGCCAGAGAAAGATGAGAAAGAAATTCATGTCAGTGGCGGTGCCAAGACGTGAAGT 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 803 TTGCTGTCGCCAGCGGGGGAACCAATGCAACATGCGGTGGTGGAAAGAGGGAAG 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 527 TCATAATGCCCTTCAGATGGGAGCCCAACCCCACTGCGCTGTGTAAGAAATGCGCAAG 586
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 863 AGTTTAAAGCAGAGATCGCATTTGAGGGCTACAAAGTACGAAACGACGTGAGCCTCA 922
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 587 AATTCAAACCTGACACAGAAATTTGAGGGCTACAAAGTCCGTTATGCACTGAGCATCA 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 923 TTATGCAAGATGTGGTCCATCTTGACAGAGGAATTAATACCTGTGTGTGAGCAATGAAT 982
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 647 TAATGACTCTGTGTGCTCTTGACAGAGGCAACTACACTTCATTTGTGAGAAATGAGT 706
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 983 ACGGGTCATCATCACTACCACTGATGTTGTGAGAGCATGCGCTCACCGGCCCA 1042

```

```

DB 707 ACGGAGCATCAACACACATACCACTGATGTGTGAGGGGTCCCTCACCGGCCCA 766
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1043 TCCTCCAAACCGGACTGCGCGCAATGCTCCACAGTGTGCGAGAGACGTAGATTGG 1102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 767 TCCTGCAACGAGCTTGGCCCGCAACAAACAGTGGCCCTGGGTGACAGCTGAGTTCA 826
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1103 TCTGCAAGTTTACATGATGATGCGCCACATCCAGTGGATGCAAGCAGTGGAAAGA 1162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 827 TGTGTAAGTGTACATGATGACCCGACACCCACATCCAGTGGTAAAGCATGAGCTGA 886
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1163 ACGGAGTAATACGGGCCCGACAGGGGCTCCCTACCTCAAGTTTCAAGGCCCGGTG 1222
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 887 ATGGGAGCAAGATTTGGCCAGAACACCTGCTATGTCAGATTTGAAGACTGCTGAG 946
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1223 TTAACACACGACAAAGAGATTGAGTTCTATATTGGAATGTAACCTTTGAGAGAG 1282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 947 TTAATACCAACCGCAAAAGAGATGAGGTCTTCACTTAAGAAATGTCCTTTGAGGAG 1006
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1283 CTGGGGAATATAGTGTGCGGGGTAATTCATTTGGATATCCTTTGACTGTGATGTG 1342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1007 CAGGGAGTATACGTGCTTGGCGGTAATCTATGCGACTTCCACTGACTGATGGT 1066
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1343 TGACAGTTCTGCCAGCGCTGGAAGAGAAAGAGATTACACTTCCCGACACTACTGG 1402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1067 TGACCGTCTGGAAGCCCTGGAAGAGAGCGCGCACTGATGACCTGCGCCCTGACTGG 1126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1403 AGATAGCAATTTACTGATAGAGGGTCTTAAATGCGCTGTATGCTGTGATACATGCC 1462
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1127 AGATCATCATCTATTGCAACAGGGGCTTCTCATCTGCTGATGGGTGCTGATCG 1186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1463 TGTGCCGATGAAGAACAGACAGCAAGACAGTTCAGACGCGCGCGGTGTCACA 1522
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1187 TCTACAGATGAAGATGATGATCCAGAGAGAGTACTTCCAGCCGAGATGCTGTGACA 1246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1523 AGCTGACCAAGATATCCCTCTGCGAGACAGTAAACATTTGCGTGAAGTCACTGCT 1582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1247 AGCTGACCAAGATATCCCTCTGCGAGACAGTAAACATTTGCGTGAAGTCACTGCT 1306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1583 CCATGAATCTCAACACCCGCTGTGTGAGATTAACAACAGCCCTCTTTCACGGCAGACA 1642
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1307 CCATGAATCTGTGGGCTTCTTGTGCTTGGCCATCAAGCGCTC-----TCTCCAGTGGGA 1360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1643 CCCCCTGCTGGAGGGGTCTCGAGTATGATTAACAGAGCCCAAAATGGAGTTTC 1702
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1361 CTCCCATGCTAGAGGGGTCTGAGTATGAGCTTCCAGAGCCCTGCTGCGAGCTGC 1420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1703 CAAGAGATTAAGTGAACATGCGGCAACCCCTGGGAGAAAGTTGCTTGGGCAAGTGTCA 1762
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1421 CTGCGGACAGAGACTGCTTAAAGCAACCCCTGGAGAGAGGGCTGTTGGGAGGTGCTG 1480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1763 TGGCGGAGCAGTGGCAATTTGACAAAGACAGCCCAAGAGCGGCTCACCTGCGCTGA 1822
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1481 TGGCAGAGGCTATCGGGCTGAGCAAGACAAACCAACGTTGTGACAAAGTGGCTGTGA 1540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1823 AGATGTTGAAGATGATGCGACAGAGAAAGACCTTCTATGCTGGTGTGAGATGAGAGA 1882
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1541 AGATGTTGAAGTGGAGAGCAAGAGAAAGACTTGTCAACCTGATCTGAAGAAATGAGA 1600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1883 TGAATGAAGTATGAGGAAACACAAAGATATCATTAATTTTGTGGAGCTGCACACAG 1942
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1601 TGAATGAAGTATGAGGAAACACAAAGATATCATTAATTTTGTGGAGCTGCACACAG 1660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1943 ATGGGCTCTCTATGTCATAGTTGACTATGCTCTAAAGGCAACTCTCGAGAAATACCTCC 2002
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1661 ATGGTCTCTTGTATGTCATGCTGAGTATGCTCCAAAGGCAACCTCGGAGTACTGCTC 1720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2003 GAGCCCGGAGCGCACCCGGGATGAGATCTCTATACATTAACCGTGTTCCTGAGGAGC 2062
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1721 AGCCCGGAGCGCCCGAGGGCTGGAATTAAGTCTTACAAACCCGACCAACCAAGAGAGC 1780
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2063 AGATGACCTTCAAGAGACTTGGTCTCATGACCTACAGCTGGCGACAGGATGAGTACT 2122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db	1781	AGCTCTCCTCCAGAGACCTGCTGCTCTCCGGCCCTACACAGTGGCCGGAGCATGGAGTATC	1840
Qy	2123	TGGCTTCCCAAAATGTATTCAATCGAGATTATAGACCCAGAAATGTTTGGTAACGAAA	2182
Db	1841	TGGCTTCCCAAGATGCTATACCCAGACCTGGACCCAGAAATGTCTGGGAGACGAGG	1900
Qy	2183	ACATGTGATGAAATATAGCAGACTTTTGGACTGGCCAGAGATATCAACAAATATAGACTAT	2242
Db	1901	ACAATGTGATGAAGATATAGCAGACTTTGGCTCGCACAGGGACATTTCCACCAATCGCACTACT	1960
Qy	2243	ACAAAAGACACCAATGGAGCGGCTCCACAGTCAAGAGATGGCTCCAGAAAGCCGTGTTG	2302
Db	1961	ATAAAAAGACACCAACGCGCCGCTCTGTGAAGGATGGCACCCAGAGGATTAATTTTG	2020
Qy	2303	ATAGACTATACACTCATCATCAGAGTATGTCTGGCTTCGGGCTGTTAATGTGGAGATCT	2362
Db	2021	ACGGAGATCTACACCCACACAGAGATGTGTGGCTTTGGGGGTGCTCCTGTGGAGATCT	2080
Qy	2363	TCACTTTAGGGGGCTGGCCCTTACCCAGGAGATTCCGCTGGAGAACTTTTAACTGTCTGA	2422
Db	2081	TCACCTTGGCGGGCTCCCTCCATACCCCGGTGTCGTGTGAGAGAACTTTTCAAGCTGTGA	2140
Qy	2423	AGGAAGGACACAGATATGAGATAAACCCAGCCCACTGCACACAGAACTGTATCATGATGATGA	2482
Db	2141	AGGAGGGTCAACCCGATGAGAACCCCAAGTATGCTACCCAAACAGGTGTATCATGATGATGC	2200
Qy	2483	GGGAGCTTTGGCATGCTAGCTGCTCCCTCCAGAGACCAACGTTCAAGAGTTGGTGAAGACT	2542
Db	2201	GGGAGCTGCTGGCATGCTAGCTGCTCCCTCAGACAGAACCCCTTCAAGAGCTGGTGGAGAGCC	2260
Qy	2543	TGGATGAAATTTCTCACTCTCACAAACCAATGAGGAATACTTGGAACTCAGCCCAACCTCTCG	2602
Db	2261	TGGACCCGATCTGTGGCCCTTCACTCCACCAACAGAGATCTGAGACTGTCACTGCCCCCTGG	2320
Qy	2603	AACGATTAATCAACTAGTTACCTCGAACAAGAAGTTCT---TGTCTTCCAGAGATGATTT	2659
Db	2321	ACCGATCTACTCCCCAGGTTTCCCGAGACCCGGAGCTCTACGTGCTCCAGAGGGAGGATTT	2380
Qy	2660	CTGTTTTCCTCCAGACCCCATCGCTTTACGAAACATGCTTCTCCTAGTATCA	2712
Db	2381	CCGCTTCTCTCATGAGCCCTCGCCGGAGAGAGCCCTGCTGCTGCCCGACACCA	2433
RESULT 13			
US-07-997-133-2			
Sequence 2, Application US/07997133			
GENERAL INFORMATION:			
APPLICANT: Bergonzoni, Laura			
APPLICANT: Mazue, Guy			
APPLICANT: Isacchi, Antonella			
APPLICANT: Roncucci, Romeo			
APPLICANT: Sarmientos, Paolo			
TITLE OF INVENTION: Extracellular Form of the Human			
TITLE OF INVENTION: Fibroblast Growth Factor Receptor			
NUMBER OF SEQUENCES: 8			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: OBION, SPIVAX, MCLELLAND, MAIER & NEUSTADT,			
ADDRESSEE: P.C.			
STREET: 1755 Jefferson Davis Highway, Fourth Floor			
CITY: Arlington			
STATE: Virginia			
ZIP: 22202			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/07/997,133			
FILING DATE: 28-DEC-1992			
CLASSIFICATION: 530			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/07/642,755			

[illegible]


```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-451-822A-14

Query Match      27.7%; Score 1180.6; DB 2: Length 2662;
Best Local Similarity 70.8%; Pred. No. 2,9e-280;
Matches 1621; Conservative 0; Mismatches 644; Indels 24; Gaps 3;

OY 458 GCCTGTTGAAGATGCCCCGCTATCATGTTGCACTAAGATGGGGTGCACCTGGGGCCCA 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 GGTGGGGAGACGATGTGACAGAGCATCACTGCTGGGGAGCGGCTGACGCTGGCGAAA 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 518 ACATAGGACAGTGTATTATGGGAGTACTTGCAGATAAAGGGCGGCGAGCCAGAGACT 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 GCACCGGCACCCGCATCACAGGGGAGAGGTGAGGTGCAGAGCTCCGTGCGCCGAGACT 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 578 CCGGCTCTATGCTTGTACTGCCAGTAGACGTGTAGACAGTGAAGTTGTACTTCAATG 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 CCGGCTCTATGCTTGTCTTAACAGCAGCCCTCGGGCAGTGCACACCTACTTCTCG 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 638 TGAATGCACAGATGCATCTCATCCGGAGATATGAGATGCACCGCATGTGCGGAG 697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 TCATATTTTCAATGCTCTCCCTCTCTCGAGAGATGATGATGATGATGATGATGATGAT 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 698 ATTTTGTGATGAGACAGTACACAA-----GAGAGCAGCATCTAGTGG 742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 494 CAGAGAGAGAAAGAAACAGATTAACACCAACCAACCGTATGCCCTGATGCTCCATATTGGA 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 743 CCACACAGAAAAAGATGAAAAAGCGGCTCCAGTCTGTGCTGCGGCCAACACTGTCAAGT 802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 CATCCCCAGAAAAAGATGAAAAAGAAATTCATGATGATGATGATGATGATGATGATGAT 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 803 TTGCGGCCAGCGGGGGGAAACCCCAATGCCAACCATGCGGTGCGTGAAGAAAGCGGAG 862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 TCMAATGCCCTTTCATGATGAGACCCCAACCCCACTGCGGTGTTGAAAAAATGGCGAAAG 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 863 AGTTTAAAGCAGAGCATCTCCATTGAGGCTACAGGTACAGAAACAGCAGCTGAGGCTCA 922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 AATTCAACCTGACCAACAAATTGGAGGCTACAGGTCCGTTATGCGCAGCTGAGACATCA 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 923 TTATGGAAGTGTGCTCCCATCTGACACAGGAAATTTATCTGTGTGTGGAGAAATGAAT 982
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 734 TATGACTCTGTGTGTGCTCTGACACAGGCAATCAACACTGATTTGTGAGAAATGAGT 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 983 ACGGTCATCATATCAGATCAGATCAGTGGATTTGTGAGAGCATGCGCTCAACGGGCCCA 1042
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 794 ACGGACGATCAACACACATACAGTGTGATGTGTGAGAGCGGTCCCTCACCGGCCCA 853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1043 TCCTCCAAACCGGAGTCCCGGAAATGCTCCACAGTGTGCGAGAGAGATGAGATTGG 1102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 854 TCCTGCAACAGAGGTTGCCCGCAACAAAAAGTGGCCCTGGTATGACACAGTGTGAGATTC 913
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1103 TCTGCAAGTTTACATGTATGCGCCAGCCCAATCCATGATGATCAAGCAACGTGGAAGA 1162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 914 TGTGTAAGTGTGATGATGACCGCAGCCGACATCCAGTGGCTAAAGCAATGAGAGTGA 973
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1163 ACGGAGTAAATACGGGCGCGAGCGGCTCCCTACTCAAGGTTTCAAGGGCGCGCGGTG 1222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 974 ATGGGAGCAAGATTTGGCCAGACACACTGCTTATGTCCAGATCTTGAAGAGCTGTGGAG 1033
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1223 TTAAACACACGAGCAAAAGATTTGAGTTCTCTATATTTCGGAATTAACCTTTTGAAGAG 1282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 TTAAATACACCGCAAAAGATGAGAGTGTCTTCACTTAAGAAATGTCTCTTTGAGAGAG 1093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1283 CTGGGGAATATACGTCTTGGGGGGGTAATTTCTATTGGAATATCTTTCACTGCTGATGT 1342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 CAGGGAGATATACGTCTTGGGGGGGTAATCTTATCGGACTCTCCCATCACTCTGCACTGT 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1343 TGACAGTTCTGCCAGCGCTGGAAGAAAGAGATTAACAGTTTCCCAAGACTACTGTGG 1402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

Db 1154 TGACCGTTCTGAAAGCCCTGGAAGAGAGGCCGCGAGTATGACTGTGCCCTTACTCTGG 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1403 AGATTAACCATTTACTGCATAGGGGCTTCTTATATGCGCTGTATGTGTATACATCATCC 1462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1214 AGATATCATATTAATTCACAGGGGCTTCTCTCATCTCTGATGATGATGATGATGATGAT 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1463 TGTGCCAATGAAGAACAGCAGCAAGAGCAAGTTCAGACAGCCAGCGGCTGTGCACA 1522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1274 TCTACAAAGATGAAGATGTGATACCAAGAGATGACTTCCAGACCCAGATGTGTGCACA 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1523 AGCTGAACCAACGTATCCCTCGGAGAGAGTAAAGTTCGTGCTGATGATGATGATGATGAT 1582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1334 AGCTGGCCAAAGACATCTCTCTGCGAGAGAGTAAACAGTGTGCTGATCCAGTGCAT 1393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1583 CCATGAACCTCCACACACCCCTGTGTAGATTAACACAGCCCTCTTCAACGGCAGACA 1642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1394 CCATGAACCTCTGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1643 CCCCATGCTGGCAGGGGCTCCAGATATGAATCTTCAGAGGACCCCAAAATGGAGATTTC 1702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1448 CTCCATGCTAGCAGGGGCTCTGATATGAGCTTCCCAAGACCTCGCTGGAGACTGC 1507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1703 CAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGGTTGCTTTGGGCAAGTGTCA 1762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1508 CTGCGGACAGACTGTCTTAGCAAAACCTCGGAGAGGCTCTTTGGGCAAGTGTGT 1567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1763 TGGCGGAGCAGTGGGAATTTGCAAAAGACAGCCCAAGAGGGGTGACCGTGGCTGA 1822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1568 TGGCAAGGCTATGCGGCTGTGAGAAAGACAAACCAACCTGTGACCAAAATGGCTGTGA 1627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1823 AGATGTTGAAGATGATGACACAGAGAAAGACCTTCTGATCTGTGTGATGATGATGATGAT 1882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1628 AGATGTTGAAGTGTGAGACGACAGAGAAAGACTTTGACACCTGATCTCAAGAAATGAGA 1687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1883 TCATGAAGTATGTTGGGAAAACACAGATATCATTAATCTTCTTGGAGCCTGCACACAG 1942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1688 TGAATGAAGTATGATCGGGAAGCATTAAGAAATATCATCAACTGCTGGGGGCTGCACAG 1747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1943 ATGGGCTCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1748 ATGTGCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2003 GAGCCGAGAGCCACCCGGGATGAGTACTCTATGACATTAACCTGTTCTCGAGAGC 2062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1808 AGGCCCCGAGAGCCCGAGGGCTGGAATFACGTACAAACCCAGCCACCAACCCAGAGAGC 1867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2063 AGATGACCTTCAAGGACTGTGTCTATGCACTACCACTGCTGCGCAGAGCATGAGTACT 2122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1868 AGCTTCTCTCAAGGACCTGTGTCTCTGCGCTACACAGGTGGCCGAGGATGAGATATC 1927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2123 TGGCTTCCCCAAAATGATTAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 2182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1928 TGGCTTCCAAGAGTGCATATACCCGAGACTGCGACCCAGAAATGTCTGTGTACAGAG 1987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2183 ACATATGATGAATAATAGCAGACTTTGACTCGCCAGAGATATCAACAATATATAGTATT 2242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1988 ACATATGATGAATAATAGCAGACTTTGACTCGCCAGAGATATCAACAATATATAGTATT 2047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2243 ACAAAAAGACCAATATGGGCGGCTTCAAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTTG 2302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2048 ATAAAAAGACCAACCAAGCGGCTGCTCTGTGAAAGTGTGACACCCGAGGATTTATTGG 2107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2303 ATAGATATACACTCATCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2108 ACCGATCTACACCCACAGAGATGATGTGTGTCTTTTCCGGGTCTCTGTGTGAGATTT 2167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2363 TCACCTTAAAGGGGCTGCGCTTACCAAGAGATTCCTGTGAGGAACTTTTAACTGTCTGA 2422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2168 TCACCTTGGGCGGCTCCCATACCCCGGTGTGTGTGAGGAACTTTTCAAGTGTCTGA 2227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2423 AGGAAGGACACAGAAATGATTAAGCCAGCACTGCACCAAGAACTGTACATGATGATGA 2482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 2228 AGAGAGTGCACCGCATGGAACAAGCCCACTAACTGCACCAACAGAGCTGTACATGATGATGC 2287
Qy 2433 GGGAGTGTGGCATGACAGTGGCCCTCCAGAGACCAAGCTTGAAGCATGGTGGAGAAGACT 2542
Db 2288 GGGAGTGTGGCATGACAGTGGCCCTCCAGAGACCAAGCTTGAAGCATGGTGGAGAAGACT 2347
Qy 2543 TGGATGCAATTCCTCACTCTCAACACCAATGAGAAATTAATGACCTTGCACCAACCTTCG 2602
Db 2348 TGGACCGCATGCTGGCTTGAACCTTCAACAGAGACTTACCTGACCTGTCCATGCCCCCTGG 2407
Qy 2603 AACAGTATTCACCTGATTAACCTGACACAAAGATTCT---TGTTCCTCAGAGATGATT 2659
Db 2408 AACAGTATTCACCTGATTAACCTGACACAAAGATTCT---TGTTCCTCAGAGATGATT 2467
Qy 2660 CAGTGTTCCTCAGACACCAACCTTACGAAACATGCTTCCTCAGATATCCACACATAA 2719
Db 2468 CCGTCTTCTCTATATGACCGCTGCGGAGAGAGCCCTGCTGCCCCGACACCAAGCCAGC 2527
Qy 2720 ACCGCAATG 2728
Db 2528 TTGCAATG 2536

RESULT 15
US-08-323-430-14
Sequence 14, Application US/08323430
Patent No. 6344546
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jare, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0496
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2662 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-323-430-14

Query Match 27.7%; Score 1180.6; DB 4; Length 2662;
Best local Similarity 70.8%; Pred. No. 2.9e-280;

Matches 1621: Conservative 0; Mismatches 644; Indels 24; Gaps 3:
Qy 458 GCCTGTTGAAGATGCGCCCGCTGATCACTGTTGAGTAAAGATGGGGTCACTTGGGGCCA 517
Db 254 GGGTGGGAGAGATGTGAGAGCATCAACTGGCTGGGAGGGGGTGGAGTGGGAA 313
Qy 518 ACAATAGACAGCTTATTTGGGAGTACTTGCAGATTAAGCGGCCCAAGCTTGAAGACT 577
Db 314 GCAACCGCACCCGATCACAGGGAGAGGTGAGGTGACAGACTCCGTCGCCACACT 373
Qy 578 CCGGCTCTATGCTTGTACTGCTGCACTGAGTGAAGTGAAGAACTTGGATCTCATGG 637
Db 374 CCGGCTCTATGCTTGTACTGCTGCACTGAGTGAAGTGAAGAACTTGGATCTCATGG 433
Qy 638 TGAATGTCAGATGCGATCTCATCCGAGATGATGAGATGACACCGATGGTGGAG 697
Db 434 TCAATGTTCAATGCTCTCCCTCTCTGAGAGATGATGATGATGATGATGATGATGAT 493
Qy 698 ATTTTGTAGTGAACAGTAAACA-----GAGAGCCACTACTGGA 742
Db 494 CAGAGAGAAAGAAACAGATTAACACCAACCAACCTATCCGCTAGCTCATATTGGA 553
Qy 743 CCAACACAGAAAGATGGAAGAAAGCGCTCATGCTGCTGCGGCGCAACCTGTCAGT 802
Db 554 CATCCCGAGAAAGATGGAAGAAAGATGATGATGATGATGATGATGATGATGATGAT 613
Qy 803 TTGCTGCGCCAGCGGGGGGAAACCAATGCCAATCCATGCGTGGTGAAGAAAGCGGAG 862
Db 614 TCAATGCGCTTCCAGTGGAGAACCCCAACCTGCGTGGTGAAGAAAGCGGAG 673
Qy 863 AGTTTAAGCAGAGCATGCTATGAGGCTACAGAGTACGAACACGACACTGAGACTCA 922
Db 674 AATTCAAACTGACCAAGAAATGGAGGCTACAGAGTCCGTTATGCCACTGAGACATCA 733
Qy 923 TTATGGAAGTGTGCTCCATCTGACAAAGGAAATTAACGTGTGGTGAAGTAAAT 982
Db 734 TTATGAGCTGTGTGCTGCTGCTGCAAGGCACTTACCTGCTATTTGGAGAAATGAGT 793
Qy 983 ACGGCTCATCAATCAACAGTACACCTGATGTTGTGAGAGCATGCGCTGACCGGCCCA 1042
Db 794 ACGGAGAGATCAACCAACATACAGTGTGATGCTGAGAGGCGCTGACCGGCCCA 853
Qy 1043 TCCTCCAAAGCGGACTGCGCGCAATGCTCCACAGTGTGGAGAGAACGTAGAGTTG 1102
Db 854 TCCTCCAAAGCGGACTGCGCGCAATGCTCCACAGTGTGGAGAGAACGTAGAGTTG 913
Qy 1103 TCTGCAAGTTTACAGTGTGCTGCGCCAGCCCAATCATCAGTGTGATCAAGCAAGTGA 1162
Db 914 TCTGTAAGTGTACAGTGTGCTGCGCCAGCCCAATCATCAGTGTGATCAAGCAAGTGA 973
Qy 1163 ACGGAGTAAATACGGGCGCCGAGCGGCTGCTTACCTCAAGGTTCTCAAGCGCGCGGTG 1222
Db 974 ATGGAGCAAGATGTGGCCGAGCAACCTGCTTATGTCCAGATCTTGAAGTGTGCGAG 1033
Qy 1223 TTAACACCAAGCAAGAGATGAGTGTCTATATTCGGAATGTAATTTTGGAGAGC 1282
Db 1034 TTAATACCAAGCAAGAGATGAGTGTCTTCAATTAATGTAATTTTGGAGAGC 1093
Qy 1283 CTGGGGAATATAGTGTGCGGCGGTAATTTATTTGATGATCTTTCCTGATGATGT 1342
Db 1094 CAGGAGATATAGTGTGCGGCGGTAATTTATTTGATGATCTTTCCTGATGATGT 1153
Qy 1343 TGACAGTTCTGCAGCGCTGGAAGAGAAAGATTAACAGCTTCCCGAGACTGCTGG 1402
Db 1154 TGACGTTCTGGAAGCGCTGGAAGAGAGCGCGGAGTATGACCTGCGCCCTGACTGG 1213
Qy 1403 AGATAGCCATTTACTGATAGAGGCTTCTTAATGCTGATGATGATGATGATGATGATG 1462
Db 1214 AGATATCATCTATTGCAACAGGCGCTTCTCATCTGCTGATGATGATGATGATGATG 1273
Qy 1463 TGTGGCGAATGAAGAACAGACCAAGAAAGCAAGACTTTCAGCGAGCGGCTGTGACA 1522
Db 1274 TCTACAGATGAAGAGTGTACCAAGAGATGATCTTCACAGCCAGATGCGCTGTGACA 1333

[illegible]

Oy	2603	AACGATNTACCAGTTACCCGTGACAACAAGATTCT---	TGTTCTTCAGAGATGATT	2659
Dd	2408	ACCGACTACTCCCCAGCTTTCGCCGACCCGGAGCCT	ACGTGCCTCCAGGGGGGATT	2467
Oy	2660	CTGATTTTTTCCGAGCCCATGCTTTAGAACATGCTTCCTCA	GTAATCACACATAA	2719
Dd	2468	CCGCTTCTTCATGAGACCGCTGCCGAGAGCCCTGCTGCCG	ACACCCAGCCGACG	2527
Oy	2720	ACGGCAGTG	2728	
Dd	2528	TTGCCAAATG	2536	

Search completed: December 11, 2002, 14:33:23
Job time : 144 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:21:12 ; Search time 120 Seconds
(without alignments)
13868.608 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268

Sequence: 1 cccaagaccactctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: .IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCIT_NEM_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCITUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4268	100.0	4268	10	US-09-954-456-293
2	4268	100.0	4268	10	US-09-954-456-1599
3	1177.2	27.6	3726	10	US-09-925-302-271
4	1130	26.5	3454	12	US-10-044-090-48
5	662.2	15.5	1451	10	US-09-917-800A-146
6	643	15.1	848	10	US-09-814-950-1
7	640.6	15.0	2184	10	US-09-728-952-82
8	502.8	11.8	514	10	US-09-867-701-4969
9	432	10.1	458	10	US-09-895-828-380
10	394.2	9.2	446	10	US-09-867-701-9869
11	319.4	7.5	422	10	US-09-960-352-6996
12	294	6.9	294	10	US-09-895-828-446
13	275.2	6.4	2782	9	US-10-108-605-250
14	271.2	6.4	33239	10	US-09-814-950-3
15	262.4	6.1	618	10	US-09-731-872-128
16	253.4	5.9	260	9	US-10-040-739-91
17	250.4	5.9	415	10	US-09-960-352-10423
18	249.4	5.8	413	10	US-09-960-352-5581
19	242	5.7	434	10	US-09-960-352-5227

c	20	237.6	5.6	410	10	US-09-960-352-4303	Sequence 4303, Ap
	21	235.6	5.5	402	10	US-09-960-352-14442	Sequence 14442, A
	22	233.6	5.5	392	10	US-09-960-352-4293	Sequence 4293, Ap
	23	232.6	5.4	391	10	US-09-960-352-2603	Sequence 2603, Ap
c	24	225.4	5.3	355	10	US-09-960-352-1177	Sequence 1177, Ap
	25	218.4	5.1	395	10	US-09-867-701-3177	Sequence 3177, Ap
	26	217.2	5.1	352	10	US-09-960-352-4640	Sequence 4640, Ap
	27	203	4.8	379	10	US-09-728-445-340	Sequence 340, Ap
	28	194	4.5	3914	12	US-10-044-090-148	Sequence 148, App
	29	192.8	4.5	5406	10	US-09-919-408-5	Sequence 5, App11
	30	192.8	4.5	5406	10	US-09-872-136-5	Sequence 5, App11
	31	192.8	4.5	5470	10	US-09-766-678-1	Sequence 1, App11
	32	181.6	4.3	366	10	US-09-960-352-10878	Sequence 10878, A
c	33	179	4.2	6827	10	US-09-982-610-17	Sequence 17, App1
	34	177.4	4.2	4425	10	US-09-982-610-31	Sequence 31, App1
	35	177.4	4.2	9108	10	US-09-982-610-45	Sequence 45, App1
	36	171.6	4.0	5084	9	US-09-954-531-1383	Sequence 1383, Ap
	37	171.6	4.0	5084	9	US-09-967-768A-277	Sequence 277, App
	38	169.4	4.0	3992	10	US-09-944-807-9	Sequence 9, App11
	39	166.8	3.9	332	10	US-09-960-352-10875	Sequence 10875, A
c	40	159.4	3.7	3270	10	US-09-866-510-1	Sequence 1, App11
	41	159.4	3.7	3270	10	US-09-866-510-3	Sequence 3, App11
	42	159.4	3.7	3270	10	US-09-866-510-5	Sequence 5, App11
	43	159.4	3.7	4054	9	US-09-955-363-35	Sequence 35, App1
	44	159.4	3.7	6378	10	US-09-919-497-40	Sequence 40, App1
	45	159.4	3.7	6412	10	US-09-769-987-1	Sequence 1, App11

ALIGNMENTS

RESULT 1
US-09-954-456-293
Sequence 293, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE OF INVENTION: Sels
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 293
LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-293
Query Match 100.0%; Score 4268; DB 10; Length 4268;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	CCCAAGGACCACTTCTCTGGGTTTGGAGTTGCTCCCCACAAACCCGGGGCTGTGGCTTTC	60
Db	1	CCCAAGGACCACTTCTCTGGGTTTGGAGTTGCTCCCCACAAACCCGGGGCTGTGGCTTTC	60
OY	61	TCCATCCGACCCACGGCGGGGGCCGGGGGACAAACACAGTCGCGGAGAGCGTTGGCATTC	120
Db	61	TCCATCCGACCCACGGCGGGGGCCGGGGGACAAACACAGTCGCGGAGAGCGTTGGCATTC	120
OY	121	AAAGTACTGCAGCAGCAGCGGGCAGCGCCCTCGGTTCTTGAGCCCAACCGAGCTGAAGCA	180
Db	121	AAAGTACTGCAGCAGCAGCGGGCAGCGCCCTCGGTTCTTGAGCCCAACCGAGCTGAAGCA	180
OY	181	TTGGCGGAGTGCATTCGGCCGCTAGAGGAAAGTGTGCAATGGGATTTAAAGCCCAATGGAGA	240
Db	181	TTGGCGGAGTGCATTCGGCCGCTAGAGGAAAGTGTGCAATGGGATTTAAAGCCCAATGGAGA	240
OY	241	TATGAAGAGAGACCGGGGATTTGGTACCGTAAACCATGTGCAAGCTGGGGGTCTTCATCTGC	300
Db	241	TATGAAGAGAGACCGGGGATTTGGTACCGTAAACCATGTGCAAGCTGGGGGTCTTCATCTGC	300
OY	301	CTGGTCGCGGTGCACATGGCAACCTTGTCCTCGGCCCGCCCTCCTTCAAGTTAATTAG	360
Db	301	CTGGTCGCGGTGCACATGGCAACCTTGTCCTCGGCCCGCCCTCCTTCAAGTTAATTAG	360
OY	361	GATACCACTATTAGACCCAGAAAGACCACCAACCAATATCAATCTCTCAACAGAAAGTG	420
Db	361	GATACCACTATTAGACCCAGAAAGACCACCAACCAATATCAATCTCTCAACAGAAAGTG	420
OY	421	TACGTGGCTGCGCCAGGGGAGTGGCTTAGAGTGTGCGCTGTGAAAGATGCCCGCTG	480
Db	421	TACGTGGCTGCGCCAGGGGAGTGGCTTAGAGTGTGCGCTGTGAAAGATGCCCGCTG	480
OY	481	ATCAGTTGAGCTAAAGATGGGGGTGCATTTGGGGCCCAACATAGACAGTGGTTATTGGG	540
Db	481	ATCAGTTGAGCTAAAGATGGGGGTGCATTTGGGGCCCAACATAGACAGTGGTTATTGGG	540
OY	541	GAGTACTTGCAGATTAAGGGCGCCAGCGCTAGAGACTCGCGCTCTATGTCTTGTACTGCC	600
Db	541	GAGTACTTGCAGATTAAGGGCGCCAGCGCTAGAGACTCGCGCTCTATGTCTTGTACTGCC	600
OY	601	AGTAGACTGTAGACACTGTAAACTTGGTACTTATGTGAATGTCAAGATCCATCTCA	660
Db	601	AGTAGACTGTAGACACTGTAAACTTGGTACTTATGTGAATGTCAAGATCCATCTCA	660
OY	661	TCCGGACATGATGAGATGACACCACCATGCTGGCGGAAGATTTTGTCAGTAGACAACGTAAAC	720
Db	661	TCCGGACATGATGAGATGACACCACCATGCTGGCGGAAGATTTTGTCAGTAGACAACGTAAAC	720
OY	721	AACAAGAGACCACTATCTGAGCCAAACACAGAAAGATGGAAGCGGCTCCATCTGTG	780
Db	721	AACAAGAGACCACTATCTGAGCCAAACACAGAAAGATGGAAGCGGCTCCATCTGTG	780
OY	781	CTGTGGGCAACACTGTCAAGTTTCGTGCGCCAGCCGGGGGGGAACCCATGCCCAACATG	840
Db	781	CTGTGGGCAACACTGTCAAGTTTCGTGCGCCAGCCGGGGGGGAACCCATGCCCAACATG	840
OY	841	CGGTGTGCTGAAGAAACGGGAGAGGATTTAAGCAGAGACATTCGATTTGGAGCTACAAAGTA	900
Db	841	CGGTGTGCTGAAGAAACGGGAGAGGATTTAAGCAGAGACATTCGATTTGGAGCTACAAAGTA	900
OY	901	CGAAACAGCACTGTGAGCTCATATTATGGAAAGTGTGTCCTATCTGACAAAGGAAATAT	960
Db	901	CGAAACAGCACTGTGAGCTCATATTATGGAAAGTGTGTCCTATCTGACAAAGGAAATAT	960
OY	961	ACCTGTGTGTGAGAATGAATACGGGTCCATCAATCAGAGTACACACTGGATGTTGTG	1020
Db	961	ACCTGTGTGTGAGAATGAATACGGGTCCATCAATCAGAGTACACACTGGATGTTGTG	1020
OY	1021	GAGGATATCGCTCAACGGGGCCCATCTCTCAAGCCGGAGCTCGGGCAAAATGCTTCCACATG	1080
Db	1021	GAGGATATCGCTCAACGGGGCCCATCTCTCAAGCCGGAGCTCGGGCAAAATGCTTCCACATG	1080

Qy	1081	GTGCGAGGAGACGTAAGAGTTTGTCGTGAGGGTTACAGTGAATGCCACGCCACATCCAG	1140
Db	1081	GTCCGAGGAGACGTAAGAGTTTGTCGTCAAGGTTTACAGTGAATGCCACGCCACATCCAG	1140
Qy	1141	TGCGATCAAGCACTGTCGAAAGAACGGCAGTAAATACGGGCCCGGACGGGCTGGCTACCTC	1200
Db	1141	TGGATTCAGGCACTGTGCAGAAAGAACGGCAGTAAATACGGGCCCGGACGGGCTGGCTACCTC	1200
Qy	1201	AAGGTTCTCAAGGCCGCCGGGTAAACACCACGGCAAGAGATTGAGGTTCTCTATATT	1260
Db	1201	AAGGTTCTCAAGGCCGCCGGGTAAACACCACGGCAAGAGATTGAGGTTCTCTATATT	1260
Qy	1261	CGGAATGTAACTTTTGGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATCTATTGGG	1320
Db	1261	CGGAATGTAACTTTTGGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATCTATTGGG	1320
Qy	1321	ATAATCCTTTCACCTCGCATGGTTGACAGTTCTCCAGGCCCTGTGAAAGAAAGAGATT	1380
Db	1321	ATAATCCTTTCACCTCGCATGGTTGACAGTTCTCCAGGCCCTGTGAAAGAAAGAGATT	1380
Qy	1381	ACAGGTTCCCCAGACACTACCTGTGAGATAGCCATTATCTGATATGGGGTCTCTTAATGCC	1440
Db	1381	ACAGGTTCCCCAGACACTACCTGTGAGATAGCCATTATCTGATATGGGGTCTCTTAATGCC	1440
Qy	1441	TGTATGTGTGAACAGTCATCTCTGTGCCGATTAAGACACGACGACAGAGCCAGACTTC	1500
Db	1441	TGTATGTGTGAACAGTCATCTCTGTGCCGATTAAGACACGACGACAGAGCCAGACTTC	1500
Qy	1501	AGCAGCCAGACGGCGCTGTGCACAAAGCTACCAAAAGTATCCCTCGGGAGAGAGATTACA	1560
Db	1501	AGCAGCCAGACGGCGCTGTGCACAAAGCTACCAAAAGTATCCCTCGGGAGAGAGATTACA	1560
Qy	1561	GTTTGGGCTGAGTCACAGCTCCCTCATGAACCTCCAAACACCCGCTGTGTAGATTAACA	1620
Db	1561	GTTTGGGCTGAGTCACAGCTCCCTCATGAACCTCCAAACACCCGCTGTGTAGATTAACA	1620
Qy	1621	CGCCCTCTCTTAACAGGGCAGACACCCCATCTGTGGCAGGGGTCTCGAGATATGAACCTCA	1680
Db	1621	CGCCCTCTCTTAACAGGGCAGACACCCCATCTGTGGCAGGGGTCTCGAGATATGAACCTCA	1680
Qy	1681	GAGGACCCCAAAATGGGATTTCCAAAGATATACCTGACACTGGGCAAGCCCTGGGAGAA	1740
Db	1681	GAGGACCCCAAAATGGGATTTCCAAAGATATACCTGACACTGGGCAAGCCCTGGGAGAA	1740
Qy	1741	GGTTGCTTTGGGCAAGTGTCTATGGCGGAAGCAGTGGGATTTGACAAAGACAAAGCCCAAG	1800
Db	1741	GGTTGCTTTGGGCAAGTGTCTATGGCGGAAGCAGTGGGATTTGACAAAGACAAAGCCCAAG	1800
Qy	1801	GAGGGGTCACCGTGGCCCGTGAAGATTTTAAAGATGATGCCACAGAGAAAGACCTTCT	1860
Db	1801	GAGGGGTCACCGTGGCCCGTGAAGATTTTAAAGATGATGCCACAGAGAAAGACCTTCT	1860
Qy	1861	GATCTGGGTGACAGAGATGGAGATGATACAGATGATTGGGAAACAAGATTTCTATAAT	1920
Db	1861	GATCTGGGTGACAGAGATGGAGATGATACAGATGATTGGGAAACAAGATTTCTATAAT	1920
Qy	1921	CTTCTTTGAGAGCTGCACACAGAGATGGGCTCTCTATGTCTATAGTTAGATGCTCTAAA	1980
Db	1921	CTTCTTTGAGAGCTGCACACAGAGATGGGCTCTCTATGTCTATAGTTAGATGCTCTAAA	1980
Qy	1981	GGCAACCTTCGAGAAATACCTCCAGGCCGAGGCCACCCGGGATGGAGTACCTTATGAC	2040
Db	1981	GGCAACCTTCGAGAAATACCTCCAGGCCGAGGCCACCCGGGATGGAGTACCTTATGAC	2040
Qy	2041	ATTAAACGCTGTTCTCGAGAGCAATATACCTTAAAGACCTTGTGTATGACCTTACAG	2100
Db	2041	ATTAAACGCTGTTCTCGAGAGCAATATACCTTAAAGACCTTGTGTATGACCTTACAG	2100
Qy	2101	CTGGCCAGAGGATGAGATATTGGCTTCCCAAAAATGTATTATCTGAGATTTAGCAGCC	2160
Db	2101	CTGGCCAGAGGATGAGATATTGGCTTCCCAAAAATGTATTATCTGAGATTTAGCAGCC	2160
Qy	2161	AGAAATGTGTTTGTGACGAAACAAATGTGTATGAAATAGCAGACTTTGACTCGCCAGA	2220

|||||
Db 2161 AGAAAGTTTGGTAACAGAAAAAATGTGATMAAATACACACTTTGGACTGCGCAGA 2220
QY 2221 GATATCAACAATATAGACTATTCAAAAAGACCAATGGGGGCTTCCAGTCAAGTGG 2280
Db 2221 GATATCAACAATATAGACTATTCAAAAAGACCAATGGGGGCTTCCAGTCAAGTGG 2280
QY 2281 ATGGCTCCAGAACCCCTGTTTGTATAGATATACACTCATCAGAGTGTCTGTGCTTC 2340
Db 2281 ATGGCTCCAGAACCCCTGTTTGTATAGATATACACTCATCAGAGTGTCTGTGCTTC 2340
QY 2341 GGGGTGTTAATGTGGAGATCTTCACTTTAGSGGGCTCGCCCTACCCAGGAGTTCCGTTG 2400
Db 2341 GGGGTGTTAATGTGGAGATCTTCACTTTAGSGGGCTCGCCCTACCCAGGAGTTCCGTTG 2400
QY 2401 GAGGACTTTTAACTGCTGGAAGGAGACACAGAAATGATATAGCCAGCACTGCACC 2460
Db 2401 GAGGACTTTTAACTGCTGGAAGGAGACACAGAAATGATATAGCCAGCACTGCACC 2460
QY 2461 AAGCACTGATCATGATGATGAGGAGACTGTTGGCATGCACTGCCCTCCAGAGCAACG 2520
Db 2461 AAGCACTGATCATGATGATGAGGAGACTGTTGGCATGCACTGCCCTCCAGAGCAACG 2520
QY 2521 TTCAAGCAGTTGTTAGAAAGACTTGATCGAATTTCTCACTCTCAACAACCAATGAGATAC 2580
Db 2521 TTCAAGCAGTTGTTAGAAAGACTTGATCGAATTTCTCACTCTCAACAACCAATGAGATAC 2580
QY 2581 TTGGACCTCAGCCCAACCTCTCGAAGACGATATTCACCTAGTTACCTGCACACAGAGTTCT 2640
Db 2581 TTGGACCTCAGCCCAACCTCTCGAAGACGATATTCACCTAGTTACCTGCACACAGAGTTCT 2640
QY 2641 TGTCTTTCAGGAGATATCTGTTTTTCTCAGACCCCATGCTTACGAACCATGCTT 2700
Db 2641 TGTCTTTCAGGAGATATCTGTTTTTCTCAGACCCCATGCTTACGAACCATGCTT 2700
QY 2701 CCTCAGTATCCACACATTAACGGCAGTGTAAACATGAATGACTGTGCTGCTGCC 2760
Db 2701 CCTCAGTATCCACACATTAACGGCAGTGTAAACATGAATGACTGTGCTGCTGCC 2760
QY 2761 CAACAGGACAGCAGTGGGAACCTAGTACAGTACAGAGGAGAGACATGCTGCCAGAGC 2820
Db 2761 CAACAGGACAGCAGTGGGAACCTAGTACAGTACAGAGGAGAGACATGCTGCCAGAGC 2820
QY 2821 TTGTTCTCTCCACTGTATATATGATGATCAGAGAGTAAATATTTGAAAAATATCAGCA 2880
Db 2821 TTGTTCTCTCCACTGTATATATGATGATCAGAGAGTAAATATTTGAAAAATATCAGCA 2880
QY 2881 TATGTGTAAGATTTTATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAGAGTT 2940
Db 2881 TATGTGTAAGATTTTATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAGAGTT 2940
QY 2941 TCTGAGACAGTGGAGTGGCCAGGCCACCTGTAACCCCTCTACCGCGCGTGTCTG 3000
Db 2941 TCTGAGACAGTGGAGTGGCCAGGCCACCTGTAACCCCTCTACCGCGCGTGTCTG 3000
QY 3001 GCTGTGAGCAGTAGAGACTCAAGGTGAGCTGCGTTCTGCCCTCTCTGTTAATTTGTAA 3060
Db 3001 GCTGTGAGCAGTAGAGACTCAAGGTGAGCTGCGTTCTGCCCTCTCTGTTAATTTGTAA 3060
QY 3061 TAATTGGAGAGATTTATGTGACACACACTTACAGAGCAAAATGACATATATAGTGC 3120
Db 3061 TAATTGGAGAGATTTATGTGACACACACTTACAGAGCAAAATGACATATATAGTGC 3120
QY 3121 TGGATGATGATTAATATATCAATTAATGATATATATATATATATATATATATTAAGAGT 3180
Db 3121 TGGATGATGATTAATATATCAATTAATGATATATATATATATATATATATTAAGAGT 3180
QY 3181 TATTTTGTATGATTTTAAATGATGATGCCAATGACCTAGAAAAATGCTGCTCTT 3240
Db 3181 TATTTTGTATGATTTTAAATGATGATGCCAATGACCTAGAAAAATGCTGCTCTT 3240
QY 3241 TTTTATAGCTATTTGCTAAATGCTGTTCTTACACATTAATTTCTTAATTTTCCACGACGA 3300
|||||

Db 3241 TTTTATAGCTATTTGCTAAATGCTGTTCTTACACATTAATTTCTTAATTTTCCAGGACA 3300
QY 3301 GAGGTGAAAAATATCTTTGCTTTCACGGAAAAATGATATACCTTAATTAATTAAT 3360
Db 3301 GAGGTGAAAAATATCTTTGCTTTCACGGAAAAATGATATACCTTAATTAATTAAT 3360
QY 3361 TGGTAATATCAAAACAAATTAATCATTTATAGTTTTTTTTTGTAAATTAAGTGCAATTTCT 3420
Db 3361 TGGTAATATCAAAACAAATTAATCATTTATAGTTTTTTTTTGTAAATTAAGTGCAATTTCT 3420
QY 3421 ATGACGACACACAGCAGACTAGTTAATCTATTGCTTGACCTTAAGTATACAGATCC 3480
Db 3421 ATGACGACACACAGCAGACTAGTTAATCTATTGCTTGACCTTAAGTATACAGATCC 3480
QY 3481 TTTGAAAAAGCAATTTTAAATATATGACTAATTTGGGAAAAATGAGTTTGATTTAT 3540
Db 3481 TTTGAAAAAGCAATTTTAAATATATGACTAATTTGGGAAAAATGAGTTTGATTTAT 3540
QY 3541 TTGTGTTTAAATGCTGCTGCACAGCATTTGCTTACACCTCCATAATGCCCATATTTAA 3600
Db 3541 TTGTGTTTAAATGCTGCTGCACAGCATTTGCTTACACCTCCATAATGCCCATATTTAA 3600
QY 3601 AAGAACTCATTTAGGAAGGTGTTCAATTTTGTGTGCAACCCGTGCATTAAGTCAACG 3660
Db 3601 AAGAACTCATTTAGGAAGGTGTTCAATTTTGTGTGCAACCCGTGCATTAAGTCAACG 3660
QY 3661 CAACGTTAAGTGGACTTCCCAAGATTAATGTAACACAGCTCTCTTAAAGATGCTTTA 3720
Db 3661 CAACGTTAAGTGGACTTCCCAAGATTAATGTAACACAGCTCTCTTAAAGATGCTTTA 3720
QY 3721 ATCCATTCCTTGAAGACAGACCTTAGTTGAATGATATGACGAATGTCCTCTGCGCA 3780
Db 3721 ATCCATTCCTTGAAGACAGACCTTAGTTGAATGATATGACGAATGTCCTCTGCGCA 3780
QY 3781 GCTGECCTTCTGCTCTGACTGCACATTAATCAGATTAACCTGATTCCTTCAGTGAAT 3840
Db 3781 GCTGECCTTCTGCTCTGACTGCACATTAATCAGATTAACCTGATTCCTTCAGTGAAT 3840
QY 3841 TTTGATTAATGGCTTCCAGACTTTTGGCTGGAAGACCCGTTAAGTACTTCAAGTCCA 3900
Db 3841 TTTGATTAATGGCTTCCAGACTTTTGGCTGGAAGACCCGTTAAGTACTTCAAGTCCA 3900
QY 3901 TCAATAGAAAAATTAACACAGAGTTGTTCTGATAGTTTGGGATATACATCTTT 3960
Db 3901 TCAATAGAAAAATTAACACAGAGTTGTTCTGATAGTTTGGGATATACATCTTT 3960
QY 3961 TTAAGGATGCTTTCATCTAATTTCTGACAGACCTCACCAAAAGATCCAGCCTCATACC 4020
Db 3961 TTAAGGATGCTTTCATCTAATTTCTGACAGACCTCACCAAAAGATCCAGCCTCATACC 4020
QY 4021 TACATCAGAAAAATATGCGCGTTGCTCTGCTACTAAAGTATGCTTTGCTTTGG 4080
Db 4021 TACATCAGAAAAATATGCGCGTTGCTCTGCTACTAAAGTATGCTTTGCTTTGG 4080
QY 4081 AAACACCACCTCACTTTGCAATAGCCGTGCAAGATGAAATGCAATTAACATGATCTTATG 4140
Db 4081 AAACACCACCTCACTTTGCAATAGCCGTGCAAGATGAAATGCAATTAACATGATCTTATG 4140
QY 4141 TGTTTACAAAATTTGAGAAAGTATTTAATAAACCTGTTAATTTTATAGTACAAATAAAA 4200
Db 4141 TGTTTACAAAATTTGAGAAAGTATTTAATAAACCTGTTAATTTTATAGTACAAATAAAA 4200
QY 4201 ATGTTTCTACAGATTTAATGTTAAGCAAGCAAAATTAAGTACGGAATTTAAAAAAA 4260
Db 4201 ATGTTTCTACAGATTTAATGTTAAGCAAGCAAAATTAAGTACGGAATTTAAAAAAA 4260
QY 4261 AAAAAAAA 4268
Db 4261 AAAAAAAA 4268

RESULT 2
US-09-954-456-1599

```
: Sequence 1599, Application US/09954456
: Patent No. US20020115057A1
: GENERAL INFORMATION:
: APPLICANT: Young, Paul
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
: FILE REFERENCE: 689290-76
: CURRENT APPLICATION NUMBER: US/09/954,456
: CURRENT FILING DATE: 2001-09-18
: PRIOR APPLICATION NUMBER: US/60/233,617
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US/60/234,052
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234,923
: PRIOR FILING DATE: 2000-09-25
: PRIOR APPLICATION NUMBER: US/60/235,134
: PRIOR FILING DATE: 2000-09-25
: PRIOR APPLICATION NUMBER: US/60/235,637
: PRIOR FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US/60/235,638
: PRIOR FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US/60/235,711
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: US/60/235,720
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: US/60/235,840
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: US/60/235,863
: PRIOR FILING DATE: 2000-09-27
: NUMBER OF SEQ ID NOS: 2276
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1599
: LENGTH: 4268
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1599
```

```
Query Match      100.0% Score 4268; DB 10; Length 4268;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CCCAAGGACACTCTCTCGGTTTGAGATTGCTCCACAAACCCGGGGCTCGCTTTC 60
DB 1 CCCAAGGACACTCTCTCGGTTTGAGATTGCTCCACAAACCCGGGGCTCGCTTTC 60
OY 61 TCCATCCGACCCAGCGGGGGCGGGGACAAACACAGGTCGCGAGAGCGTTGCCATTTC 120
DB 61 TCCATCCGACCCAGCGGGGGCGGGGACAAACACAGGTCGCGAGAGCGTTGCCATTTC 120
OY 121 AAGTGACTGACAGCAGCAGCGCGAGCGGCTTCGTTCTGAGCCACCGCAGAGGCTGAAGCA 180
DB 121 AAGTGACTGACAGCAGCAGCGCGAGCGGCTTCGTTCTGAGCCACCGCAGAGGCTGAAGCA 180
OY 181 TTCCGGGTAGTCATGCCGTAGAGAGAGTGTCAGATGGATTAAAGTCCACATGGAGA 240
DB 181 TTCCGGGTAGTCATGCCGTAGAGAGAGTGTCAGATGGATTAAAGTCCACATGGAGA 240
OY 241 TATGGAAGAGACCGGGATTGGTACCTTACCATTGTCAGCTGGGGTGTTCATCTGC 300
DB 241 TATGGAAGAGACCGGGATTGGTACCTTACCATTGTCAGCTGGGGTGTTCATCTGC 300
OY 301 CTGGTGTGTGTACCATGCGCAACCTTGTCCCTGGCCGCCCTCTTCAGTTAGTTGAG 360
DB 301 CTGGTGTGTGTACCATGCGCAACCTTGTCCCTGGCCGCCCTCTTCAGTTAGTTGAG 360
OY 361 GATACCAATTAGAGCCAGAGAGCCACCAACCAATATACCAAAATCTCTAACCAAGAG 420
DB 361 GATACCAATTAGAGCCAGAGAGCCACCAACCAATATACCAAAATCTCTAACCAAGAG 420
OY 421 TAGGTGCTGTCCGCCAGAGGAGTGTAGAGGTTCGCTGCTTGTGAAGATGCCGCCGTG 480
```

```
DB 421 TAGGTGCTGTCCGCCAGAGGAGTGTAGAGGTGCGCTGCTGTTGAAGATGCCGCCGTG 480
OY 481 ATACAGTGGACATAAGATGGGGTGCACCTTGGGGCCCAACAATAGACACTGCTATTGGG 540
DB 481 ATACAGTGGACATAAGATGGGGTGCACCTTGGGGCCCAACAATAGACACTGCTATTGGG 540
OY 541 GAGTACTTCAGATTAAGAGGCGCCAGCCCTAGAGACTCCGGCCCTATGCTTACTGGC 600
DB 541 GAGTACTTCAGATTAAGAGGCGCCAGCCCTAGAGACTCCGGCCCTATGCTTACTGGC 600
OY 601 AGTAGAGCTGTAGACAGTGAACCTTGTCTCATGTGATGTCACAGATGCCATCTCA 660
DB 601 AGTAGAGCTGTAGACAGTGAACCTTGTCTCATGTGATGTCACAGATGCCATCTCA 660
OY 661 TCCGGAGATGATGAGATGATACACCGATGGTGGGGAAGATTTTGTCTAGTGAAGACATAAC 720
DB 661 TCCGGAGATGATGAGATGATACACCGATGGTGGGGAAGATTTTGTCTAGTGAAGACATAAC 720
OY 721 AACCAAGAGACCACTACTGAGACCAACACAGAAAGATGGAAGAGCGGCTCCATGCTGTG 780
DB 721 AACCAAGAGACCACTACTGAGACCAACACAGAAAGATGGAAGAGCGGCTCCATGCTGTG 780
OY 781 CCGCGGCCCAACACTGTCAAGTTTCGTCGCCAGCGGGGGGAACCCAAATGCCAACCATG 840
DB 781 CCGCGGCCCAACACTGTCAAGTTTCGTCGCCAGCGGGGGGAACCCAAATGCCAACCATG 840
OY 841 CGGTGGCTGAAAAACGGGAAGGTTTAAGCAGAGACATTCGCTTGGAGCTTCAAGGTA 900
DB 841 CGGTGGCTGAAAAACGGGAAGGTTTAAGCAGAGACATTCGCTTGGAGCTTCAAGGTA 900
OY 901 CGAAACCAACACTGTGAGACCTCATTTATGAAAGTGTGTCCATCTGACAAAGGAATTAAT 960
DB 901 CGAAACCAACACTGTGAGACCTCATTTATGAAAGTGTGTCCATCTGACAAAGGAATTAAT 960
OY 961 ACCTGTGTGTGTGAGATGAATACGGGTCATCAATCACACGTACCACTGTGATGTTGTG 1020
DB 961 ACCTGTGTGTGTGAGATGAATACGGGTCATCAATCACACGTACCACTGTGATGTTGTG 1020
OY 1021 GAGCGATCGGCTTACCGGGCCATCCCTCCAAAGCCGGGACTCGGGCAATATGCTTCACAGTG 1080
DB 1021 GAGCGATCGGCTTACCGGGCCATCCCTCCAAAGCCGGGACTCGGGCAATATGCTTCACAGTG 1080
OY 1081 GTGCGAGAGACGTAGAGTTTGTCTCAAGGTTTACAGTATGCCCCAGCCCAATCCAG 1140
DB 1081 GTGCGAGAGACGTAGAGTTTGTCTCAAGGTTTACAGTATGCCCCAGCCCAATCCAG 1140
OY 1141 TGGATCAACGACGTGAAAAAAGAACGCGAGTAAATACGGGCCCGACGGCTGCGCTACCTC 1200
DB 1141 TGGATCAACGACGTGAAAAAAGAACGCGAGTAAATACGGGCCCGACGGCTGCGCTACCTC 1200
OY 1201 AAGGTTCTCAAGGCCCGCGGTGTTAAACACACGAGCAAAAGAGATTAGGTTCTCTATATT 1260
DB 1201 AAGGTTCTCAAGGCCCGCGGTGTTAAACACACGAGCAAAAGAGATTAGGTTCTCTATATT 1260
OY 1261 CGGAATGTAACTTTTGAAGCGCTGGGGAATATAGCTGCTGGCGGTAATTCATTTGGG 1320
DB 1261 CGGAATGTAACTTTTGAAGCGCTGGGGAATATAGCTGCTGGCGGTAATTCATTTGGG 1320
OY 1321 ATATCTTTTCACTCTCATATGTTGACAGTTTTCGCCAGCCCTGGAAAGAGAAAGAGATT 1380
DB 1321 ATATCTTTTCACTCTCATATGTTGACAGTTTTCGCCAGCCCTGGAAAGAGAAAGAGATT 1380
OY 1381 ACAAGTTCGCCAGACTACTGAGATAGCATTTACTGCATAGGGGTCTTCTTAATGCC 1440
DB 1381 ACAAGTTCGCCAGACTACTGAGATAGCATTTACTGCATAGGGGTCTTCTTAATGCC 1440
OY 1441 TGTATGTTGTAAAGTCAATCTGTGCGGAATGSAACAACGACCAAGAAAGCAGACTTC 1500
DB 1441 TGTATGTTGTAAAGTCAATCTGTGCGGAATGSAACAACGACCAAGAAAGCAGACTTC 1500
OY 1501 ACGAGCCAGCGGCTGTGCAAGGTGACCAAGCTATCCCTCGCGAGACAGGTAA 1560
DB 1501 ACGAGCCAGCGGCTGTGCAAGGTGACCAAGCTATCCCTCGCGAGACAGGTAA 1560
```

Db 1501 AGCAGCCAGCGGGCTGTGCACAGCTGACCAAAAGTATCCCTCGGAGACAGTTAAC 1560
Qy 1561 GTTGGCTGAGTCCAGCTCTCATGAATCCCAACACCCGCTGGTGAATTAACACA 1620
Db 1561 GTTGGCTGAGTCCAGCTCTCATGAATCCCAACACCCGCTGGTGAATTAACACA 1620
Qy 1621 GCGCTCTCTTCAAGGCGACACACCCCATGCTGGCAGGGGTCTCGAGTATGAATCTCA 1680
Db 1621 GCGCTCTCTTCAAGGCGACACACCCCATGCTGGCAGGGGTCTCGAGTATGAATCTCA 1680
Qy 1681 GAGGACCCCAAAATGGGAGTTTCCAAAGATTAAGCTGACCTGGCAAGCCCTGGAGAA 1740
Db 1681 GAGGACCCCAAAATGGGAGTTTCCAAAGATTAAGCTGACCTGGCAAGCCCTGGAGAA 1740
Qy 1741 GGTCTCTTGGGCAAGTGGTCAATGGCGGAAGCAAGTGGCAATTAAGCAAGGCCAAG 1800
Db 1741 GGTCTCTTGGGCAAGTGGTCAATGGCGGAAGCAAGTGGCAATTAAGCAAGGCCAAG 1800
Qy 1801 GAGGCGGTACCCGTGGCGGTGAAGATGTTGAAAGATGATGACACAGAGAAAGCCTTCT 1860
Db 1801 GAGGCGGTACCCGTGGCGGTGAAGATGTTGAAAGATGATGACACAGAGAAAGCCTTCT 1860
Qy 1861 GATCGGTGTCAAGATGAGATGATGAAGATGATGGGAAACACAAAGATTCATAAT 1920
Db 1861 GATCGGTGTCAAGATGAGATGATGAAGATGATGGGAAACACAAAGATTCATAAT 1920
Qy 1921 CTCTCTGAGCCTGACACAGAGATGGGCTCTATGTCATAGTTGATGATCCCTTAA 1980
Db 1921 CTCTCTGAGCCTGACACAGAGATGGGCTCTATGTCATAGTTGATGATCCCTTAA 1980
Qy 1981 GGCACCTCCGGAATACCTCCGAGCCGAGGCCACCCGGATGAGATCTCATATGAC 2040
Db 1981 GGCACCTCCGGAATACCTCCGAGCCGAGGCCACCCGGATGAGATCTCATATGAC 2040
Qy 2041 ATTAACCGTGTCCGAGAGAGATGACCTTCAAGAGATTTGGTGTCAATGACCTACAG 2100
Db 2041 ATTAACCGTGTCCGAGAGAGATGACCTTCAAGAGATTTGGTGTCAATGACCTACAG 2100
Qy 2101 CTGGCAGAGGCGATGAGTACTTGGCTTCCCAAAATGATTCATGAGATTTAGCAGCC 2160
Db 2101 CTGGCAGAGGCGATGAGTACTTGGCTTCCCAAAATGATTCATGAGATTTAGCAGCC 2160
Qy 2161 AGAATGTTTTGTTGTAACGAAAAACATGATGAATAATGACAGCTTTGACTCCCAAA 2220
Db 2161 AGAATGTTTTGTTGTAACGAAAAACATGATGAATAATGACAGCTTTGACTCCCAAA 2220
Qy 2221 GATATCACAATATAGACTATTACAAAAAGACCAACATGGGCGCTTCCACTCAAGTGG 2280
Db 2221 GATATCACAATATAGACTATTACAAAAAGACCAACATGGGCGCTTCCACTCAAGTGG 2280
Qy 2281 ATGCTCCAGAAAGCCCTGTTGATAGAGATATACACTCATCAGAGTATGCTGTCTTC 2340
Db 2281 ATGCTCCAGAAAGCCCTGTTGATAGAGATATACACTCATCAGAGTATGCTGTCTTC 2340
Qy 2341 GGGGTGTTAATGTGGAGATCTTCACTTTAGGGGCTGCGCTACCCAGGATTTCCCGTG 2400
Db 2341 GGGGTGTTAATGTGGAGATCTTCACTTTAGGGGCTGCGCTACCCAGGATTTCCCGTG 2400
Qy 2401 GAGGAACCTTTTAACTGCTGAAGAGACACAGATGATTAAGCCAGCCAACTGCACC 2460
Db 2401 GAGGAACCTTTTAACTGCTGAAGAGACACAGATGATTAAGCCAGCCAACTGCACC 2460
Qy 2461 AAGCAACTGTATGATGATGAGGAGCTGTGGCATGCGAGTGCCTCCAGAGACCAAG 2520
Db 2461 AAGCAACTGTATGATGATGAGGAGCTGTGGCATGCGAGTGCCTCCAGAGACCAAG 2520
Qy 2521 TTCAAGCAAGTTGGTGAAGAGCTGGAATTCACCTCTACAAACCAATAGGAATAC 2580
Db 2521 TTCAAGCAAGTTGGTGAAGAGCTGGAATTCACCTCTACAAACCAATAGGAATAC 2580
Qy 2581 TTGGAACCTCAGCAACCTCTGGAACAGATTACACTAGTTACCTGACAGAAAGTTCT 2640
Db 2581 TTGGAACCTCAGCAACCTCTGGAACAGATTACACTAGTTACCTGACAGAAAGTTCT 2640

Qy 2641 TGTCTTCAGAGATGATTCGTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTT 2700
Db 2641 TGTCTTCAGAGATGATTCGTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTT 2700
Qy 2701 CCTCAGTATCCACATTAACGGCAGTGTAAAAACATGAATAGTGTCTGCTGTCC 2760
Db 2701 CCTCAGTATCCACATTAACGGCAGTGTAAAAACATGAATAGTGTCTGCTGTCC 2760
Qy 2761 CAACAGGACAGACTGGGAACTTACCTAAGTACAGAGGAGACCATGCTCCAGAC 2820
Db 2761 CAACAGGACAGACTGGGAACTTACCTAAGTACAGAGGAGACCATGCTCCAGAC 2820
Qy 2821 TTGTTGCTCCACTGTTATATATGATCAGAGAGTAATTAATTTGGAAAAATACAGA 2880
Db 2821 TTGTTGCTCCACTGTTATATATGATCAGAGAGTAATTAATTTGGAAAAATACAGA 2880
Qy 2881 TATGTATAAGATTTATACAGTTGAAAACTGTAAATCTTCCAGAGAGAGAAAGTT 2940
Db 2881 TATGTATAAGATTTATACAGTTGAAAACTGTAAATCTTCCAGAGAGAGAAAGTT 2940
Qy 2941 TCTGAGCAGTGGACTGCCAAGCCACATGTAACCCCTTCACCTGCGCTTCTG 3000
Db 2941 TCTGAGCAGTGGACTGCCAAGCCACATGTAACCCCTTCACCTGCGCTTCTG 3000
Qy 3001 GGTGGACCACTAGGACACAGTGGAGTGGCGCTTCCCTGCTTAAATTTTGTAA 3060
Db 3001 GGTGGACCACTAGGACACAGTGGAGTGGCGCTTCCCTGCTTAAATTTTGTAA 3060
Qy 3061 TAATGGAGAAATTTATGTCAGCACACACTTAACAGACACAAATGACATATATAGTGC 3120
Db 3061 TAATGGAGAAATTTATGTCAGCACACACTTAACAGACACAAATGACATATATAGTGC 3120
Qy 3121 TGGATGATGTAATATATATTCAAATATATATATATATATATATATATATATAT 3180
Db 3121 TGGATGATGTAATATATATTCAAATATATATATATATATATATATATATATATAT 3180
Qy 3181 TATTTTGTATGATTTTAAATGATGTCGCCAATGACCTTGAATAATGGTCTGCTT 3240
Db 3181 TATTTTGTATGATTTTAAATGATGTCGCCAATGACCTTGAATAATGGTCTGCTT 3240
Qy 3241 TTTTAAATGATTTTGTAAATGCTGTTCTTACATAATTTCTTAATTTACCGAGCA 3300
Db 3241 TTTTAAATGATTTTGTAAATGCTGTTCTTACATAATTTCTTAATTTACCGAGCA 3300
Qy 3301 GAGGTGGAAAAATFACCTTTGCTTTCAGGAAAAATGATTAACGTTAATTAATAAT 3360
Db 3301 GAGGTGGAAAAATFACCTTTGCTTTCAGGAAAAATGATTAACGTTAATTAATAAT 3360
Qy 3361 TGGTAATATACAAACAAATTAATCAATTAATGATTTTGTAAATTAAGGCAATTTCT 3420
Db 3361 TGGTAATATACAAACAAATTAATCAATTAATGATTTTGTAAATTAAGGCAATTTCT 3420
Qy 3421 ATGACAGGCGACACAGACTAGTTAATCTATGCTGTGACTTAACATGATCC 3480
Db 3421 ATGACAGGCGACACAGACTAGTTAATCTATGCTGTGACTTAACATGATCC 3480
Qy 3481 TTTGAAAAAGAAATTTTACATATATGACTAATTTGGGAAAAATGAAGTTTGAATAT 3540
Db 3481 TTTGAAAAAGAAATTTTACATATATGACTAATTTGGGAAAAATGAAGTTTGAATAT 3540
Qy 3541 TTGTGTTTAAATGCTGCTGACAGATGTTCTTAAGACCTGCTAAATGCCCATATTA 3600
Db 3541 TTGTGTTTAAATGCTGCTGACAGATGTTCTTAAGACCTGCTAAATGCCCATATTA 3600
Qy 3601 AAGAACTCATATATAGAAAGTGTTCATTTTGGTGCACCCGTGATTAAGCTCAACG 3660
Db 3601 AAGAACTCATATATAGAAAGTGTTCATTTTGGTGCACCCGTGATTAAGCTCAACG 3660
Qy 3661 CAAGCTTAACCTGGAATCCCAAGATTAATGTTACAGGCTCTTAAAGATGCTTAA 3720
Db 3661 CAAGCTTAACCTGGAATCCCAAGATTAATGTTACAGGCTCTTAAAGATGCTTAA 3720

Qy	3721	ATCATTCCTTTGAGGACAGACCTTATTGTAAATGATAGCAAAATGGCTTCCTGCGCA	3780
Db	3721	ATTCATTCTCTTGAGGACAGACCTTACTTGAATGATAGCAGATGTGCTTCTCTGGCA	3780
Qy	3781	GCTGGCCTTCCTGCTTCGTGAGCTTGCACATTAATCAGATTAGCCCTGATTCCTTCAGTGAAT	3840
Db	3781	GCTGGCCTTCCTGCTTCGTGAGCTTGCACATTAATCAGATTAGCCCTGATTCCTTCAGTGAAT	3840
Qy	3841	TTTTCATTAATGGCTTCCAGACTCTTTTCCGTTTGGAGACGCGCTGTAGGATCTTCAAGTCCA	3900
Db	3841	TTTTCATTAATGGCTTCCAGACTCTTTTCCGTTTGGAGACGCGCTGTAGGATCTTCAAGTCCA	3900
Qy	3901	TCATAGAAATTTGAAACACAGAGATGTTCGTCGATAGTTTGGGATACGTCATCTTT	3960
Db	3901	TCATAGAAATTTGAAACACAGAGATGTTCGTCGATAGTTTGGGATACGTCATCTTT	3960
Qy	3961	TTAAGGATTCCTTCATCTTAATTCGCGAGACGCTCACCAAAATCATCAGCCTCATAC	4020
Db	3961	TTAAGGATTCCTTCATCTTAATTCGCGAGACGCTCACCAAAATCATCAGCCTCATAC	4020
Qy	4021	TACATCAGACAAAATATCGCCGTTGTTCCCTTCGTACTAAGATATTGTCTTTGCTTTGG	4080
Db	4021	TACATCAGACAAAATATCGCCGTTGTTCCCTTCGTACTAAGATATTGTCTTTGCTTTGG	4080
Qy	4081	AAACACCCACTCACTTTTGCATATGCGCGTGAAGATCAATGAGATTTACATGATCTTATG	4140
Db	4081	AAACACCCACTCACTTTTGCATATGCGCGTGAAGATCAATGAGATTTACATGATCTTATG	4140
Qy	4141	TGTTACAAAATTTGCGAGAAACTATTATTAAACCTGTAAATTTTATCTGCATAATAA	4200
Db	4141	TGTTACAAAATTTGCGAGAAACTATTATTAAACCTGTAAATTTTATCTGCATAATAA	4200
Qy	4201	ATGTTTCTACAGATATTAAATGTTTAAACAAGCAAAATAAATGTCACGCAACTTAAAAAAA	4260
Db	4201	ATGTTTCTACAGATATTAAATGTTTAAACAAGCAAAATAAATGTCACGCAACTTAAAAAAA	4260
Qy	4261	AAAAAAAA 4268	
Db	4261	AAAAAAAA 4268	
RESULT 3			
US-09-925-302-271			
: Sequence 271, Application US/09925302			
: Patent No. US20020044941A1			
: GENERAL INFORMATION:			
: APPLICANT: Rosen et al.			
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			
: FILE REFERENCE: PA104			
: CURRENT APPLICATION NUMBER: US/09/925,302			
: PRIOR APPLICATION NUMBER: PCT/US00/05918			
: PRIOR FILING DATE: 2000-03-08			
: PRIOR APPLICATION NUMBER: 60/124,270			
: PRIOR FILING DATE: 1999-03-12			
: NUMBER OF SEQ ID NOS: 896			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 271			
: LENGTH: 3726			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc feature			
: LOCATION: (2586)			
: OTHER INFORMATION: n equals a,t,g, or c			
: NAME/KEY: misc feature			
: LOCATION: (3523)			
: OTHER INFORMATION: n equals a,t,g, or c			
: NAME/KEY: misc feature			
: LOCATION: (3664)			
: OTHER INFORMATION: n equals a,t,g, or c			
: NAME/KEY: misc feature			
: LOCATION: (3687)			

[illegible]

Dh 976 GCCTTCATCTCCTGCATGGTGGGGTGGTCTCTACAGATGAAGATGGTACC 1035
Qy 1486 AAGAGCCAGACTTTCAGCAGCCGGCTGTGCAGAACTGACCAAGATATCCCTG 1545
Dh 1036 AAGAGATGACTTCCAGAGCCAGATGGCTGTGCAGAACTGACCAAGATATCCCTG 1095
Qy 1546 CGGACAGAGTAACTGTTGGGTGATGTCAGCTCTCCATGAATCCGAACCCCGTG 1605
Dh 1096 CGCAGACAGTAACTGTTGGGTGATGTCAGCTCTCCATGAATCCGAACCCCGTG 1155
Qy 1606 GTGAGATAAACAACAGCTCTCTCAACAGCAGACACCCCATCTGGCAGGGTCTCC 1665
Dh 1156 GTTGGCCATACGGCTCTCTCCAGT-----GGGACTGCATCTAGCAGGGTCTCT 1209
Qy 1666 GAGTATGAATCTTCAGAGAGCCCAAAATGGAGTTTCCAGAGATTAAGCTGACCTGGGC 1725
Dh 1210 GAGTATGAGCTTCCGAAAGACCTCTGCGAGCTGCTCGGAGACAGACTGCTTAAAGC 1269
Qy 1726 AAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCTATGGCGGAAGCAGTGGGAATGAC 1785
Dh 1270 AAACCCCTGGGAGAGGCTGCTTTGGCAGGTGTGTGGCAGAGGCTATCGGGCTGGAC 1329
Qy 1786 AAAGCAAGCCCAAGAGAGCGGTCTACCTGGCCGTGAAGATGTTAAAGATGATCCACA 1845
Dh 1330 AAGGCAAAACCCCAAGCGGTGTGACCAAAAGTGTGAAAGATGTTAAAGTCCGACCAACA 1389
Qy 1846 GAGAAAGACCTTTCTGATCTGTGTCTCAGAGATGAGATGATGAATGATGGAAGAAC 1905
Dh 1390 GAGAAAGACCTTTCTGATCTGTGTCTCAGAGATGAGATGATGAATGATGGAAGAAC 1449
Qy 1906 AAGATATCATTAATCTTCTTGGAGCTTCACACAGATGGGCTCTCTATGCTATGATT 1965
Dh 1450 AAGATATCATTAATCTTCTTGGAGCTTCACACAGATGGGCTCTCTATGCTATGATT 1509
Qy 1966 GAGTATGCTCTAAAGAGACCTCCGAGATTAATCTCCGAGCCGAGCCACCCCGGATG 2025
Dh 1510 GAGTATGCTCTCAAGAGGCAACCTCGGGAGTACTGCAAGGCCGAGGCCCCGAGGCTG 1569
Qy 2026 GAGTATGCTCTCAAGAGGCAACCTCGGGAGTACTGCAAGGCCGAGGCCCCGAGGCTG 2085
Dh 1570 GAGTATGCTCTCAAGAGGCAACCTCGGGAGTACTGCAAGGCCGAGGCCCCGAGGCTG 1629
Qy 2086 TCATGCACTTACAGCTGCGCAGAGGATGAGTACTTGGCTTCCCAAAATGATTCAT 2145
Dh 1630 TCCTGCGCTTACAGGAGGCGCCGAGGATGAGTACTTGGCTTCCCAAAATGATTCAT 1689
Qy 2146 CGAGATTAGAGCCAGAAATGTTTGTGAACAGAAACAAATGATTAACAGAC 2205
Dh 1690 CGAGCTTGGAGCCAGAAATGTTTGTGAACAGAAACAAATGATTAACAGAC 1749
Qy 2206 TTTGACTTCCGAGAGATATCAAAATATAGACTTATCAAAAGAACCAATGGGCG 2265
Dh 1750 TTTGCTTCCGAGAGATATCAAAATATAGACTTATCAAAAGAACCAATGGGCG 1809
Qy 2266 CTTCAGTCAAGTGAATGCTTCAGAGCCCTGTTTGAATAGATATACATCAGAT 2325
Dh 1810 CTGCTTGTGAAGTGAATGCTTCAGAGCCCTGTTTGAATAGATATACATCAGAT 1869
Qy 2326 GATGCTGCTTGGGGGTGTTAATGAGGATCTTCACTTAAAGGGGCTCGCCCTAC 2385
Dh 1870 GATGCTGCTTGGGGGTGCTTGTGGAGATCTTCACTTGGGGGCTCGCCCTAC 1929
Qy 2386 CCAGGATTTCCGCTGGAGAACTTTTAAAGCTGTGAAGGAGAGACAGAAATGATTAAG 2445
Dh 1930 CCCGCTGTGCTGTGAAGAACTTTTAAAGCTGTGAAGGAGAGACAGAAATGATTAAG 1989
Qy 2446 CCAGCAACTGACCAAGAACTGTATGATGATGAGGAGCTTTGGCATGCACTGCC 2505
Dh 1990 CCCAATACTGACCAAGAGCTGTATGATGATGAGGAGCTGTGCACTGCACTGCC 2049
Qy 2506 TCCGCAACCAAGTGTAAAGAGTTGTAGAGACTTGAATGCAATTCACCTCTACA 2565
Dh 2050 TCACAGAGACCACTTCAAGAGCTGTGAAGAGCTGAGCCGATCTGTGCTTGAAC 2109

Qy 2566 ACCAATGAGAACTTGTGACCTCAGCCAACTCTGAAACAGATTAATTCACCTAGTACCCT 2625
Dh 2110 TCCAAACGAGAACTTGTGACCTCAGCCAACTCTGAAACAGATTAATTCACCTAGTACCCT 2169
Qy 2626 GACACAGAAGTCT--TGTCTTCAGAGAGATGATGTTGTTTCTTCACAGCCCATG 2682
Dh 2170 GACAAACGAGAGCTTACGTCCTCAGAGGAGAGATTCGCTCTCTCATATGAGCGGCTG 2229
Qy 2683 CCTTACGAACATGCTTCTCTCATATCCACAGATTAACGCACTG 2728
Dh 2230 CCGGAGAGCCCTGCTGCTCCCGACACCCAGCCAGCTTGGCAATG 2275

RESULT 4
US-10-044-090-48
: Sequence 48, Application US/10044090
: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: CURRENT FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: PERL Program
: SEQ ID NO 48
: LENGTH: 3454
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. US20020137081A1 493848CB1
: NAME/KEY: unsure
: LOCATION: 2, 9, 16, 39, 42, 68, 143, 268
: OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-48

Query Match 26.5%; Score 1130; DB 12; Length 3454;
Best Local Similarity 72.4%; Pred. No. 5.4e-257;
Matches 1495; Conservative 0; Mismatches 561; Indels 9; Gaps 2;

Qy 667 GATGATGAGATGACACCGATGTCGGAAGATTTTGTCTAGTGAAGACGTAACAAG 726
Dh 244 GATGATGATGATGATCTCTCTTCANAGAGAAAGAAAGAGATTAACCAACCAACCC 303
Qy 727 AGAGCAACATCTGACCAACACAGAAAGATGAAAGGCGCTCATGCTGTGCTGCG 786
Dh 304 GTAGCTCATATTGGACATCCCAAGAAAGATGAAAGAAATGTCATGCACTGCCGCT 363
Qy 787 GCCAAGCTGTCAGTTTCGCTGCGCCAGCCGGGGGAAACCCAAATGCCAACTGGCGTG 846
Dh 364 GCCAAGCAAGTAAATGTCAAATGCGCTTCAGTGGGACCCCAACCCCACTGGCGTG 423
Qy 847 CTGAAAAACGGGAAGAGCTTTAAGCAGAGCATTCGATTTGAGGCTAGCAAGTACGAAC 906
Dh 424 TTGAAAAATGGCAAGAAATTCAAACCTGACCAACAATTTGAGGCTACAGGTCCGTTAT 483
Qy 907 CAGCACTGAGGCTCTATTATGAAAGTGTGCTCCATCTGACAAAGGAATTAATACCTGT 966
Dh 484 GCCACCTGTGAGCATTAATGACTCTGTGTGTCCTCTGACAAAGGCAACTACATGTC 543
Qy 967 GTGGGGAAGATTAAGGGGTCAATCAATCAAGTACACCTGAGATGTTTGTGAAGCA 1026
Dh 544 ATTTGGGAAGATTAAGGGGTCAATCAATCAAGTACACCTGAGATGTTTGTGAAGCG 603
Qy 1027 TCGCCTACCGGCCCATCTCTCAAGCCGAGCTCGGGAAGATGCTTCCACATGCTGCGA 1086
Dh 604 TCCCTCACCGGCCCATCTCTCAAGCAGAGGTTGCCGCCCAAAACAGTGGCCCTGGGT 663
Qy 1087 GGAGACGTAGAGTTTGTGCAAGGTTTACAGTATGCCCAAGCCCAATCCAGTGTGATC 1146
Dh 664 AGCAACGTGAGATTCATGTTAAGGTGTACAGTACCCGACCCGACATCTCAGTGGCTA 723

1147 AAGCAGTGGAAAAAGACGGCAGTAAATACGGGCCGACGGGCTCCCTACCTCAAGTT 1206
1148 AAGCAGTGGAAAAAGACGGCAGTAAATACGGGCCGACGGGCTCCCTACCTCAAGTT 1206
1207 CTCAAGGCCCGCGGTGTTAAACACGACGACAAAGATTGAGCTTCTATATTCGGAAT 1266
1208 CTCAAGGCCCGCGGTGTTAAACACGACGACAAAGATTGAGCTTCTATATTCGGAAT 1266
1267 GTAACCTTTGAGGAGCGTGGGGAATATACGCTTGGCGGGAATCTTATTCGGAATTC 1326
1268 GTAACCTTTGAGGAGCGTGGGGAATATACGCTTGGCGGGAATCTTATTCGGAATTC 1326
844 GTCTCTTTGAGGAGCGTGGGGAATATACGCTTGGCGGGAATCTTATTCGGAATTC 903
1327 TTTCACTCTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1386
1328 TTTCACTCTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1386
904 CATCACTCTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 963
1387 TCCCAAGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1446
964 TCCCAAGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1023
1447 GTGTAAGAGTATCTGTCGCGGATGTAAGAAACAGACGACGACGACGACGACGAC 1506
1024 GTGTAAGAGTATCTGTCGCGGATGTAAGAAACAGACGACGACGACGACGACGAC 1083
1507 CAGCGGCTGTGACACAGCTGACACGATATCCCTGCGGAGACAGGTAACGATTTG 1566
1084 CAGATGCTGTGACACAGCTGACACGATATCCCTGCGGAGACAGGTAACGATTTG 1143
1567 GCTGAGTCCAGCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATG 1626
1144 GCTGAGTCCAGCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATG 1200
1627 TCTTCAAGGAGACACCGGCTGCTGCGGAGGATCTCGGATGATGATGATGATGATG 1686
1201 ---TCTTCAAGGAGACACCGGCTGCTGCGGAGGATCTCGGATGATGATGATGATG 1257
1687 CCAAAATGGAGTTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1746
1288 CCGTCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
1747 TTTGGGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1806
1318 TTTGGGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
1807 GTACCGGTGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1866
1378 ACCAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1437
1867 GTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1926
1438 ATCTCAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
1927 CGAGGCTGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1986
1498 GGGGCTGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
1987 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2046
1558 CTGGGGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1617
2047 CTGTTCTCTGAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2106
1618 CACAACCCAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
2107 AGAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2166
1678 CCAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1737
2167 GTTTGGTAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2226
1738 GTCTGTGACAGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797

2227 AACATATAGACTATTTACAAAAAGACCAATGGGCGGCTTCCAGTCAAGTGGATGCT 2286
1798 CACACATGAGTACTATTTAAAAAGACCAATGGGCGGCTTCCAGTCAAGTGGATGCT 1857
2287 CCAGAGCCCTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2346
1858 CCGGAGCATTTATTTGACCGGATGATGATGATGATGATGATGATGATGATGATGATG 1917
2347 TTAATGAGGAGTCTTACCTTATGAGGCGTCCCTTCCAGGATGATGATGATGATGATG 2406
1918 GTCTGTGAGATCTTCACTGAGGCGTCCCTTCCAGGATGATGATGATGATGATGATG 1977
2407 GTTTTAACTGCTGTAAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATG 2466
1978 GTTTTAACTGCTGTAAGAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATG 2037
2467 CTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2526
2038 CTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2097
2527 CAGTTGGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2586
2098 CAGTTGGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2157
2587 CTCAACCAACCTCTGCAACAGATGATGATGATGATGATGATGATGATGATGATGATG 2643
2158 GTTTCAGATGCTGTAAGAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATG 2217
2644 TCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2703
2218 TCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2277
2704 CAGTATCCACATTAACGCGAGT 2728
2278 GCACACCAACCGCAGCTTCCCATG 2302

RESULT 5
US-09-917-800A-1466
Sequence 1466, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elshoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1466

[illegible]

QY	937	-CTTCCTCCAGTGGGACCCCCCATCTAGCTGCTGTCTCTGAATATGACCTCCCTGAAC	995
QY	1685	ACCCCAAAATGGAGATTTCACAAGATAACTGACACTGGGCAACCCCTGGGAGAAAGTT	1744
Db	996	ATCCCTGCTGAGAGCTGCCCCGACAGACTGGTCTTAAAGAAAAACGGCTTGGCAAG--	1052
QY	1745	GCTTTGGCGAAGTGGTCATGGCCGAGCAAGTGGGAATTGACAAAGCAAGCCCAAGAGG	1804
Db	1053	GCTTGGGCGAGGTGGTATTGGGCCAAAGCCATCGTGTGGATAAGGACAAACCCACCGCA	1112
QY	1805	CGGTACCCCTGGGCGCTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCGATC	1864
Db	1113	TGACCAAAAGTGGGAGAGAAAGATGTTGAAGCTAATGAACAGAGAAAGACCTTCAGACC	1172
QY	1865	TGCTGTCAAGATGAGATGATGAGATGATGGGAATGGGAACCAAGAAATATCATAAATCTTC	1924
Db	1173	TGATCTCGGAGATGGAGATGATGAAATGATACCCGGGAAGCAAGAATATCATTAATCTGC	1232
QY	1925	TGGAGACCTTGCACACAGGATGGGCCCTCTATGTCATAGTGGATGATGCCCTTAAAGGCA	1984
Db	1233	TGGGGGTGTGCACCCAGAGATGATTCCTCTATGTCAATCGTGGATTATGCCCCCAAGGCA	1292
QY	1985	ACCTCCGAGATTAACCTCCGAGCCCGGAGGCCACCCGGAGTGAAGTACTCTATGACATTA	2044
Db	1293	ATCTTTGGAGATCTGACAGGCCCGGAGGCTCTCGGCTGGAGTATTGGTACAGCCCCA	1352
QY	2045	ACCGTGTCTTGAAGAGGAGATGACCTTCAAGACACTTGGTGTATGACACTACCAGCTGG	2104
Db	1353	GCCACACACCCCGAGAACGCTGTCTTCCAAAGATCGTGTCTGTGCTATTCAGTGG	1412
QY	2105	CCAGAGCGATGAGTACTTGGCTTCCCAAAATGATTTTC	2143
Db	1413	TCTGGGGCATGGAGTATCTTGCCCTCAAGAGTTTATAC	1451
RESULT 6			
US-09-814-950-1			
Sequence 1, Application US/09814950			
Patent No. US20020137130A1			
GENERAL INFORMATION:			
APPLICANT: WEI, Ming-Hui et al			
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,			
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND			
FILE REFERENCE: CLO01174			
CURRENT APPLICATION NUMBER: US/09/814, 950			
CURRENT FILING DATE: 2001-03-23			
NUMBER OF SEQ ID NOS: 4			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 1			
LENGTH: 848			
TYPE: DNA			
ORGANISM: Human			
US-09-814-950-1			
Query Match			
Best Local Similarity 15.1%; Score 643; DB 10; Length 848;			
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	86	GGGACAACACAGGTGCGCGGAGAGCGCTTGCCATTCAAAGTACGACGACGACGCGGACG	145
Db	2	GGGACAACACAGTCCGCGSAGAGACCTTGCCATTCAAGTACTGACGACGACGCGGACG	61
QY	146	GCCTCGTTCTTGAGCCCAACGCGAGGCTGAAGGCATTGGCGCGTAGTCATGCCCCGTAGAG	205
Db	62	GCCTCGTTCTTGAGCCCAACGCGAGGCTGAAGGCATTGGCGCGTAGTCATGCCCCGTAGAG	121
QY	206	GAAAGTGTGAGATGGGATTAACGTCACATGCAATGCAATGGAAGAGAGACCGGGATTGGTA	265
Db	122	GAAAGTGTGAGATGGGATTAACGTCACATGCAATGGAATGGAAGAGACCGGGATTGGTA	181
QY	266	CCGTAAACCATGGTCAAGCTGGGGTCTGTTTCATGTCGCTGTGCGGTGACCATGGCAACT	325

Db 182 CCGTAACATGCTGACGTGGGGCTGTTTCATCTGCCGTGCTGTCACCATGGCACTT 241
Qy 336 TGTCCCTGCCCCGGCCCTCTCACTTTAGTTAGATACCAATAGCCAGAAAGC 385
Db 242 TGTCCCTGCCCCGGCCCTCTCACTTTAGTTAGATACCAATAGCCAGAAAGC 301
Qy 386 CACCAACCAATACCAATCTCTCAACCAAGATAGTGGTGGTGGCCAGGGAGTGGC 445
Db 302 CACCAACCAATACCAATCTCTCAACCAAGATAGTGGTGGTGGCCAGGGAGTGGC 361
Qy 446 TAGAGGTGCGCTGCTGTTGAAGATGCGCGCTGATGATGAGTGAAGTGGGTGC 505
Db 362 TAGAGGTGCGCTGCTGTTGAAGATGCGCGCTGATGATGAGTGAAGTGGGTGC 421
Qy 506 ACTTGGGGGCCCAACAAATAGAGAGTGTATTGTTGGGAGTACTTGCAGATTAAGGGCGCA 565
Db 422 ACTTGGGGGCCCAACAAATAGAGAGTGTATTGTTGGGAGTACTTGCAGATTAAGGGCGCA 481
Qy 566 CCGCTAGAGACTCCGGCTCTATGCTTGTACTGCGCAGTACACTGTACACAGTGAACCTT 625
Db 482 CCGCTAGAGACTCCGGCTCTATGCTTGTACTGCGCAGTACACTGTACACAGTGAACCTT 541
Qy 626 GGTACTTATGTTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGTACACCG 685
Db 542 GGTACTTATGTTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGTACACCG 601
Qy 686 ATGGTGGGAAGATTTTGTCACTGAGAACAGTAAACAAAGAG 728
Db 602 ATGGTGGGAAGATTTTGTCACTGAGAACAGTAAACAAAGAG 644

RESULT 7

US-09-728-952-82
Sequence 82, Application US/09728952
Patent No. US2002011302A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Wang, Jian-Rui
APPLICANT: Yamazaki, Vicki
APPLICANT: Ujwal, Manusha L.
APPLICANT: Dimanac, Radoje T.
TITLE OF INVENTION: No. US2002011302A1el Nucleic Acids and
FILE REFERENCE: 799
CURRENT APPLICATION NUMBER: US/09/728, 952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PL-FL-genes Version 2.0
SEQ ID NO 82
LENGTH: 2184
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (40)..(2124)
US-09-728-952-82

Query Match 15.0%; Score 640.6; DB 10; Length 2184;
Best Local Similarity 73.3%; Pred. No. 1e-138;
Matches 836; Conservative 0; Mismatches 299; Indels 6; Gaps 1;

Qy 1554 GGTAAACAGTTTGGCTGAGTCCAGTCTCTCATGACTGCAACACCCGCTGGTAGAGAT 1613
Db 963 GGTCAAGGTGTCTCGAGTCCACACCGCTCATGAGCTCCACACACACACTGTGTCGAT 1022
Qy 1614 AACACAGCGCTCTTCAAGCGCAGACACCCCATGGTGGAGGGGCTCCGAGATAGA 1673
Db 1023 CCGAAGGCTGTCTCA-----GGGAGGGGCCACGCGCCCAATGTCTCCGAGCTGA 1076

Qy 1674 ACTTCAGAGAGACCCAAATGGAGATTTCAGAGATAGCTGACACTGGCCAAAGCCCT 1733
Db 1077 GCTGCTGCCCAACCCCAATAGGAGCTGTCTGGGCCGGGTGACCCCTGGGCAAGCCCT 1136
Qy 1734 GGGAGAGGTTGCTTTGGGCAAGTGTCTATGGCGAACCACTGGGAATTGGCAAGCA 1793
Db 1137 TGGGAGGGCTGTCTTGGCCAGAGTGTCTATGGAGGCCAATGGCATTTGACAAAGACCG 1196
Qy 1794 GCCAAGGAGCGGTACACCGTGGCGTGAAGATGTTGAAGATGATGCCACAGAAAGA 1853
Db 1197 GGGCCCAAGCGCTGTACACCGTGAAGATGATGATGATGATGATGATGATGATGATGAT 1256
Qy 1854 CCTTCTGATCTGTGTGAGAGATGAGATGATGATGATGATGATGATGATGATGATGAT 1913
Db 1257 CCTGTGGACCTGTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1316
Qy 1914 CATAAATCTTCTTGGAGGCTGCACACAGATGGGCTCTCATATGATGATGATGATGAT 1973
Db 1317 CATCAACCTGCTGGGCGCTGCACAGAGGGGGGCGCCCTGTACGTGTGTGAGATGATG 1376
Qy 1974 CTCTAAAGGCAACCTCCGAGAAATACCTCCAGGCCGAGGCCACCGGAGTGAATCTC 2033
Db 1377 GGCCAAAGGTAACTGCGGAGATTCTCGGGCGGGGGCGCCCGGGGCTGTGACTACTC 1436
Qy 2034 CTATGACATTAACCGTGTCTGAGAGACAGATGACCTTCAAGGACTTGTGTCTATGCA 2093
Db 1437 CTTCGACACCTGCAAGCGCCGAGAGACACTCACTTCAAGGACTGTGTCTGTGC 1496
Qy 2094 CTACAGCTGGCGAGAGCATGAGATGATGATGATGATGATGATGATGATGATGATGAT 2153
Db 1497 CTACAGCTGGCGAGAGCATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1556
Qy 2154 AGCAGCCAGAAATGTTTGGTAAACAGAAACAAATGATGAAATAGCAGACTTTGAGCT 2213
Db 1557 GCGTCCCGCATGT 1616
Qy 2214 CCGCAGAGATATCAACATATAGACTATTACAAAAGACCAACCAATGGGCGCTTCCAGT 2273
Db 1617 GCGCCGGAGCGTGCACAACTGTGACTACAAAGAAACCAACGAGCGGCTCCCGT 1676
Qy 2274 CAAGTGAATGGCTCCAGAAAGCCCTTGTGATGATGATGATGATGATGATGATGATGAT 2333
Db 1677 GAAGTGAATGGCTCCAGAAAGCCCTTGTGATGATGATGATGATGATGATGATGATGAT 1736
Qy 2334 GTCTTCCGGGCTTAAATGTGAGAGATCTCACTTAAAGGGCTGCGCCCTACCGAGGAT 2393
Db 1737 GTCTTCCGGGCTTAAATGTGAGAGATCTCACTTAAAGGGCTGCGCCCTACCGAGGAT 1796
Qy 2394 TCCGCTGAGCAACTTTTAACTGCTGAGAGAGACAGACAGATGATGATGATGATGAT 2453
Db 1797 CCTGTGAGAGGCTCTTCAAGCTGTGAAAGAGGCGCACCGCATGAGCAAGCCGCCAA 1856
Qy 2454 CTGCACCAACGAACGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2513
Db 1857 CTGCACCAACGAACGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1916
Qy 2514 ACCAAGTTCAAGAGTGTGAGAGACTGATGATGATGATGATGATGATGATGATGATGAT 2573
Db 1917 GCCACCTTTCAAGAGCTGT 1976
Qy 2574 GGAATACCTTGACCTACACCACTCTCGAAGCATTTACCTACTTACCTGACCAAG 2633
Db 1977 CGAGTACCTTGACCTGT 2036
Qy 2634 AAGTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2693
Db 2037 CAGCTTCAGCTCTCAGGAGAGACTCGGTGTTCCTCCACGACCTGTGTGTGTGTGTGTGT 2096
Qy 2694 A 2694
Db 2097 A 2097


```
RESULT 8
US-09-867-701-4969/c
; Sequence 4969, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jones, Robert
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4969
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4969
```

```
Query Match
Best Local Similarity 11.8%; Score 502.8; DB 10; Length 514;
Matches 507; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 2862 ATTGAAAGTAAATCATATGCTAAGATTATACAGTGAAGAACTGTATCTTC 2921
DB 514 ATTCGAAAGTAAATCCGATATGTAAGATTATACAGTGAAGAACTGTATCTTC 455
QY 2922 CCAGGAGGAGAACAGGTTCTGAGACGTGACCTGCCACAGCCACATGTAACCCCTC 2981
DB 454 CCAGGAGGAGAACAGGTTCTGAGACGTGACCTGCCACAGCCACATGTAACCCCTC 395
QY 2982 TCACCTGCCGTGCTGCTGCTGACACAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3041
DB 394 TCACCTGCCGTGCTGCTGCTGACACAGTGAAGTGAAGTGAAGTGAAGTGAAGT 335
QY 3042 TTCCTGTTAATTTTGTAAATTTGAGAAAGTTATGTCAGACACACTTACAGACAC 3101
DB 334 TTCCTGTTAATTTTGTAAATTTGAGAAAGTTATGTCAGACACACTTACAGACAC 275
QY 3102 AATGAGATATAGTGTGCTGATGTATTAATATATATTCAAATATATATATATA 3161
DB 274 AATGAGATATAGTGTGCTGATGTATTAATATATATTCAAATATATATATATA 215
QY 3162 TTATATATTACAGAGTATTTTGTATTTAATGATGTCCTCCATGACCT 3221
DB 214 TTATATATTACAGAGTATTTTGTATTTAATGATGTCCTCCATGACCT 155
QY 3222 AGAAATGTGCTCTCTCTTTTAAATAGTATTTGCTAAATGCTGTCTTACATAT 3281
DB 154 AGAAATGTGCTCTCTCTTTTAAATAGTATTTGCTAAATGCTGTCTTACATAT 95
QY 3282 TCTTATTTTACAGCAGAGAGTGAAGAAATCTTTGCTTCCAGGAAATGATATA 3341
DB 94 TCTTATTTTACAGCAGAGAGTGAAGAAATCTTTGCTTCCAGGAAATGATATA 35
QY 3342 CGTTAATTTTAAATTTGTAATATACAAA 3375
DB 34 CGTTAATTTTAAATTTGTAATATACAAA 1
```

```
RESULT 9
US-09-895-828-380
; Sequence 380, Application US/09895828
; Patent No. US20020099012A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Carter, Darrick
; APPLICANT: Henderson, Robert A.
```

```
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.539
; CURRENT APPLICATION NUMBER: US/09/895,828
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 380
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 371
; OTHER INFORMATION: n = A,T,C or G
US-09-895-828-380
```

```
Query Match
Best Local Similarity 10.1%; Score 432; DB 10; Length 458;
Matches 454; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
```

```
QY 3466 CTAGTATACAGATCCTTTGAAAGAGATATTTACAATATATGACTAATTTGGGAAAT 3525
DB 1 CTAGTATACAGATCCTTTGAAAGAGATATTTACAATATATGACTAATTTGGGAAAT 60
QY 3526 GAAGTTTGAATTTTGTGTTTAAATGCTGCTGCTGACAGATTTGTTAGACCTCTTA 3585
DB 61 GAAGTTTGAATTTTGTGTTTAAATGCTGCTGCTGACAGATTTGTTAGACCTCTTA 120
QY 3586 AATGCCCATATTTAAAGAACTCATATAGAGAGTGTATTTGTTGTTGCTGCAACCT 3645
DB 121 AATGCCCATATTTAAAGAACTCATATAGAGAGTGTATTTGTTGTTGCTGCAACCT 180
QY 3646 GTCATTTAGTCAAGCAAGCTGTAACTGACTTCCCAAGATTAATGTTACAGGCTCTC 3705
DB 181 GTCATTTAGTCAAGCAAGCTGTAACTGACTTCCCAAGATTAATGTTACAGGCTCTC 240
QY 3706 TTAAAGATGCTTAAATCAATTCCTTGAGACAGACCTTGTGAATGATAGCAATG 3765
DB 241 TTAAAGATGCTTAAATCAATTCCTTGAGACAGACCTTGTGAATGATAGCAATG 300
QY 3766 TGCCTCTCTGCGAGCTGCTCTCTCTGAGTTGCACATTAATGATAGCTG- 3824
DB 301 TGCCTCTCTGCGAGCTGCTCTCTCTGAGTTGCACATTAATGATAGCTG- 360
QY 3825 ATTCCTCTCAGTAATTTGATATATGCTTCCAGACTCTTT-GCGTGGAGAGCCCTGT 3883
DB 361 ATTCCTCTCAGTAATTTGATATATGCTTCCAGACTCTTTGGCGTGGAGAGCCCTGT 420
QY 3884 AGGATCTTCAAGTCCCATCATAGAAATTTGAACACA 3920
DB 421 AGGATCTTCAAGTCCCATCATAGAAATTTGAACACA 457
```

```
RESULT 10
US-09-867-701-9869/c
; Sequence 9869, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9869
; LENGTH: 446
; TYPE: DNA
```


Sequence 250, Application US/10108605
Patent No. US20020160934A1

GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stem, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
FILE REFERENCE: 3113B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 250
LENGTH: 2782
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-10-108-605-250

Query Match 6.4% Score 275.2; DB 9; Length 2782;
Best Local Similarity 59.3% Pred. No. 5.4e-54;
Matches 547; Conservative 0; Mismatches 333; Indels 42; Gaps 3;

QY 1650 GCTGGCAGGGCTCTCCGAGTATGACTTCCAGAGACCCAAATGGAGTTCCAAAGAGA 1709
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1246 GCCGGCTCCATTCAATGAATATGAATTTCCACTGAGACTCCAACTGGGAACTGCCAGAG 1305
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1710 TAAGCTGACACTGGGCGAAGCCCTGGGAGAAGCTTCTTGGGCAAGTGTCTATGCGCGA 1769
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1306 TCATTGGTACTGGGCGCCACTTTGGGAGGAAGGTGCTTTGGAGCAATGTCATGGCGGA 1365
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1770 ACCAGTGGGAATTGGANAAAGACAAGCCCAAGGAGGCGGTCAACCTGGCCGTGAAGATGTT 1829
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1366 GGTCA-----ATTAATGCCATTGTCCCGTGAATAATGTT 1398
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1830 GAAAGATGATGCGCACAGAAAGACCTTCTGATCTGCTGCACAGATGAGATGATGAA 1889
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1399 GAAAGAGAGACACAGGATGATGACATTTGCCAGCTTGGTGGGGAATGGAAGTATGAA 1458
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1890 GATGATGGGAAACACAGAATATCATAAATCTTCTTGGAGCCCTGCCAATAATACCT 1949
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1459 GATCAATTTGGGCGCATATCATATTAATTAACCTACTTGGTTGCTGACATCAAAATGTCTC 1518
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1950 TCTCTATGTCATATGTTGAGTATGCTCTTAAAGCAACCTCCGAAATATACCT 2000
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1519 GCTCTATGATTTGTTGAGTATGCTCCGCACACGGAAATCTCAAGAGACCTCTATAGGAA 1578
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2001 ---CCGAGCCCGGAGGCCACCCGGGATGAGTACTCTCTATGACATTTAACCGTGTCTCTGA 2057
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1579 TGGCCGATCCGGAAGGATCAGACACAGGACAGTCTCCGACACCGCCGCGCATGCCACCGC 1638
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2058 GGAGCAGATGACCTTCAAGGACTTGGTGCATGCACCTTACAGCTGCGCAGAGCGCATGGA 2117
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1639 TCATGATTAACCGAAGGATCTGATCAATATTGGCCOACCAAAATTTGCCAGAGGAATGGA 1698
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2118 GTACTTTGGCTTCCCAAAATGTATTATCGAGATTTAGCAGCCAGAAATGTTTTGTAAAC 2177
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1699 CTATTGGGCTCGCGCGATGCATCCATCGAATTTGGCAACGAGATCTGCTGTGAG 1758
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2178 ACAAACATGATGATGAATAATAGACAGACTTGGAGCTGGCCGAGAGATTAACAATATAGA 2237
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1759 CGATGATTTATGCTCTAAGATTTGCTGATTTTGGAGCTGGCGGAGATATCAAAAGCAGGA 1818
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2238 CTATTACAAAAGACCACCAATGGCGGCTTCCAGTCAAGTGAATGCTTCAGAAAGCCCT 2297
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1819 TTACTATCGGAAGAACAGCAATGGCAGGCTACCCATCAAAATGATGGCAGCGGATCGCT 1878
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2298 GTTTGATAGATATACACTCATCAGAGTGAATGTCTGCTCTTCCGGGCTGTTAAATGTGGGA 2357

[illegible]

```
; GENERAL INFORMATION:
; APPLICANT: Dumas Mline Edwards, Jean Baptiste
; APPLICANT: Bouquelarel, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.053.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 128
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 179..427
; NAME/KEY: s19_peptide
; LOCATION: 179..298
; OTHER INFORMATION: Von Heljne matrix
; OTHER INFORMATION: score 7.72883276007822
; OTHER INFORMATION: seq CLVVVTMTLSLA/RP
US-09-731-872-128
```

```
Query Match 6.1% Score 262.4; DB 10; Length 618;
Best Local Similarity 99.6% Pred. No. 2.3e-51;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 120 CAAGTACTGCAGCAGCAGCGCGCCCTCGGTTCTGTAGCCCGCAGCGCTGAAGC 179
DB 82 CCAGTACTGCAGCAGCAGCGCGCGCCCTCGGTTCTGTAGCCCGCAGCGCTGAAGC 141
OY 180 ATTGCGCGTAGTCATGCCCCGTAGAGGAAGTGTGCAGATGGATTAACTCCACATGAG 239
DB 142 ATTGCGCGTAGTCATGCCCCGTAGAGGAAGTGTGCAGATGGATTAACTCCACATGAG 201
OY 240 ATATGGAAGAGACCGGGGATTGTACCGTAACCATGTGCAGCTGGGGTCTTTCATCTG 299
DB 202 ATATGGAAGAGACCGGGGATTGTACCGTAACCATGTGCAGCTGGGGTCTTTCATCTG 261
OY 300 CCTGCTGCTGTACCATGGCAACCTTGTCCCTGGCGGCCCTCCTCATTAGTTAGTGA 359
DB 262 CCTGCTGCTGTACCATGGCAACCTTGTCCCTGGCGGCCCTCCTCATTAGTTAGTGA 321
OY 360 GGATACCACTTAGAGCCAGAGA 383
DB 322 GGATACCACTTAGAGCCAGAGA 345
```

```
Search completed: December 11, 2002, 17:40:36
Job time : 388 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:19:57 ; Search time 3671 Seconds
(without alignments)
18829.294 Million cell updates/sec

Title: US-09-954-556-3
Perfect score: 4268
Sequence: 1 cccaagaccacccctctcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	840.6	19.7	885 14	B0438964
2	765.6	17.9	833 9	A1127918
3	762.8	17.9	803 9	AU132307
4	731.4	17.1	987 14	B0879891
5	707.4	16.6	834 12	BG698600
6	688.2	16.1	747 9	A1081876

C	7	686.8	16.1	755 9	A1436212
C	8	680.4	15.9	823 14	BM792391
C	9	675.6	15.8	692 9	A1433805
C	10	675	15.8	690 14	BM970064
C	11	670.8	15.7	712 10	AV726725
C	12	666	15.6	693 14	B0575816
C	13	664.6	15.6	850 13	B1661597
C	14	664	15.6	787 13	B1661662
C	15	663.2	15.5	852 13	B1853362
C	16	660.4	15.5	693 12	BF059273
C	17	660.4	15.5	771 13	B1558778
C	18	658.6	15.4	786 13	B1092661
C	19	657.8	15.4	965 13	B1659067
C	20	657.4	15.4	826 13	B1658887
C	21	653.4	15.3	707 9	AT885536
C	22	651.8	15.3	799 13	BG915910
C	23	651.4	15.3	887 12	BG864512
C	24	650.8	15.2	801 13	B1558552
C	25	649.4	15.2	808 12	BG864499
C	26	647	15.2	673 12	BG706936
C	27	645.8	15.1	909 13	B1658471
C	28	644.4	15.1	767 13	B1655009
C	29	644.4	15.1	838 13	B1656679
C	30	644	15.1	815 13	B1653807
C	31	643.4	15.1	1013 13	B1656483
C	32	640.6	15.0	757 13	B1853625
C	33	640	15.0	794 13	B1661736
C	34	639	15.0	861 14	B0931738
C	35	638.6	15.0	830 13	B1558258
C	36	637	14.9	894 13	B1662081
C	37	634	14.9	770 13	BG973797
C	38	633.8	14.9	1000 13	B1656544
C	39	633.4	14.8	805 13	B1661788
C	40	632.6	14.8	791 13	BG974925
C	41	631.8	14.8	635 14	BM793028
C	42	631.6	14.8	770 13	B1656261
C	43	630.2	14.8	772 12	BG426972
C	44	630	14.8	746 13	BG974620
C	45	629.4	14.7	663 14	B0446665

ALIGNMENTS

RESULT 1
B0438964
LOCUS B0438964 885 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7761624 NIH_MGC_70 Homo sapiens CDNA IMAGE:6018096
5' mRNA sequence.
ACCESSION B0438964
VERSION B0438964.1 GI:21178040
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 885)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: LMNL13218 row: h column: 01
High quality sequence stop: 770.
Location/Qualifiers
1. 885

FEATURES
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="6018096"
/clone_lib="NIH-MGC_70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Pancreas; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

```

QY	2160	CAGAAATGTTTTGGTATACACAAAAACAATGATGAAATAATAGCAACTTTGGACTGCCAG	2213
Db	1	CAGAAATGTTTTGGTAAACACAAAAACAATGATGAAATAATAGCAACTTTGGACTGCCAG	60
QY	2220	AGATATCAACAATATATAGACTATTACAAAAAGACCAATATGGGCGGCTTCACGTCAAGTG	2279
Db	61	AGATATCAACAATATATAGACTATTACAAAAAGACCAATATGGGCGGCTTCACGTCAAGTG	120
QY	2280	GATGGCTCCAGAAAGCCCTGTTTTGATAGAGTATATACATCTATCAGAGTGAATGTCTGGTCTT	2339
Db	121	GATGGCTCCAGAAAGCCCTGTTTTGATAGAGTATATACATCTATCAGAGTGAATGTCTGGTCTT	180
QY	2340	CGGGGTGTTAATGTGGGAGATCTTTCACCTTAGGGGGCTCGCCCTACCCAGGGATTCGGCT	2399
Db	181	CGGGGTGTTAATGTGGGAGATCTTTCACCTTAGGGGGCTCGCCCTACCCAGGGATTCGGCT	240
QY	2400	GGAGGAACCTTTTAACTGCTGTAAGAGAGACACAGATATGATTAAGCCAGCCCACTGCAC	2459
Db	241	GGAGGAACCTTTTAACTGCTGTAAGAGAGACACAGATATGATTAAGCCAGCCCACTGCAC	300
QY	2460	CAACGAACCTGACATGATGATGAGGAGACTGTTGGCATGCGAGTGGCCCTCCAGAGACCAAC	2519
Db	301	CAACGAACCTGACATGATGATGAGGAGACTGTTGGCATGCGAGTGGCCCTCCAGAGACCAAC	360
QY	2520	GTTTCAAGCAGTTGGTATAGAACACTTTGGATCGAATTCTCACTCTCACACCAATATGAGAAATA	2579
Db	361	GTTTCAAGCAGTTGGTATAGAACACTTTGGATCGAATTCTCACTCTCACACCAATATGAGAAATA	420
QY	2580	CTTGAGCACTCAGCCACACCTCTGCACACAGTATTCACCTAGTTACCTTGACACACAGATTTC	2639
Db	421	CTTGAGCACTCAGCCACACCTCTGCACACAGTATTCACCTAGTTACCTTGACACACAGATTTC	480
QY	2640	TTGTGTTCTTCAGAGAAATATCTGTTTTTTCTCCAGACCCCAATGCGCTTATGAAACCAATGCT	2699
Db	481	TTGTGTTCTTCAGAGAAATATCTGTTTTTTCTCCAGACCCCAATGCGCTTATGAAACCAATGCT	540
QY	2700	TCCTCACTATCCACACATTAACGGCAGTGTAAACATGAATGACTGTCTGTGCTGTCC	2759
Db	541	TCCTCACTATCCACACATTAACGGCAGTGTAAACATGAATGACTGTCTGTGCTGTCC	600
QY	2760	CCAAGACGAGACACACTGGGAACCTAGCTATACACTAGCAGGAGAGACATGCTCTCCAGAG	2819
Db	601	CCAAGACGAGACACACTGGGAACCTAGCTATACACTAGCAGGAGAGACATGCTCTCCAGAG	660
QY	2820	CTTGTGTTCTCCACCTTGTAATATATATGATCAGAGAGTAATTAATTGGAAAAAGTATATCAGC	2879
Db	661	CTTGTGTTCTCCACCTTGTAATATATATGATCAGAGAGTAATTAATTTGGAAAAAGTATATCAGC	720
QY	2880	ATATGTCTAAAGATTTATATACAGTTGAAAACTTGTAATCTTTCCCAAGAGAG--AGAAAGAG	2937
Db	721	ATATGTCTAAAGATTTATATACAGTTGAAAACTTGTAATCTTTCCCAAGAGAGAGAAAGAG	780
QY	2938	GTTTCTTGAGACATGTGACATGCCACACAGCCACATATGAACTCTCTACACTGCGCTGTCT	2997
Db	781	TTTTTCTTGACACATGTGACATGCCACACAGCCACATATGAACTCTCTCAACTGCGCTGTCTA	840

QY 2998 CAGCGCTGTCGACCACTAGACATCCAAAG-7GCAAGCTGCGCTTC 3037
|||||
Db 841 TTGGCTGTGACCACTAGAGACTCAAGGTGACGTGCGTTC 881
|||||

RESULT 2
A1127918/c
LOCUS
DEFINITION
A1127918 833 bp mRNA linear EST 27-OCT-1998
gdc6609.x1 Soares.pregnant.uterus.NHPHU Homo sapiens cDNA clone
IMAGE:1712704.3' similar to gb:M87770 F1BRBRLAST GROWTH FACTOR
RECEPTOR 2 PRECURSOR (HUMAN);, mRNA sequence.
A1127918
A1127918.1 GI:3596432
EST.
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 833)
NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 757 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
1..833

QY	2593	CGACCTCTCGAAGACATATTCACCTAGTTACCGCTGCACAGCAAGAAAGTTCTTGTTCCTTCAGGA	2652
DB	647	GTAGAGACACTTGATGATTCGAATTCCTCCTCTCACACCAATGAGGAACTTGGACCTCAGC	588
QY	2533	GTAGAGACACTTGATGATTCGAATTCCTCCTCTCACACCAATGAGGAACTTGGACCTCAGC	2592
DB	707	ATGATGATGAGGAGGACTGGTGGCATGCTACATGCTCCCTCCAGAGCAACGTTCAAGCAGTTG	648
QY	2473	ATGATGATGAGGAGGACTGGTGGCATGCTACATGCTCCCTCCAGAGCAACGTTCAAGCAGTTG	2532
DB	767	AGCTCTCTAAGAAAGACACAGAAATGATTAAGCCAGCAACATGCAACCAAGCAACTTGTAC	708
QY	2414	AGCTGCTGAGAGACGACACAGATGATTAAGCCAGCAACATGCAACCAAGCAAC-TGTAA	2472
DB	827	GGAGATCTTCACATTTAGGGGGCGCTGCCCTACCCAGGATTTTCCGGTGGAGGAACTTTTAA	768
QY	2355	GGAGATCTTCACATTTAGGGGGCGCTGCCCTACCCAGGAG-GATTCCCGCTGGAGGAACTTTTAA	2413
QY	Best Local Similarity	97.9%: Pred. No. 7.2e-152:	3:
Matches	807: Conservative	0: Mismatches 14: Indels	3: Gaps 3:

Db	587	CAACCTCTCGAACACGATTCACCTAGTTACCTGTGACACACAAAGATTCTTGTCTTCAGGA	528
QY	2653	GATGATTCGTGTTTTTCTTCAGAGACCCCATGCGCTTAGCAACCATGGCTTCTTCAGTATCCA	2712
Db	527	GATGATTCGTGTTTTTCTTCAGAGACCCCATGCGCTTAGCAACCATGGCTTCTTCAGTATCCA	468
QY	2713	CACATTAACGGG - AAGTTAAACATGAAATGACTGTGTGCTGTGCCCTGCCCAACAGGACA	2771
Db	467	CACATTAACGGGAGGTTAAACCATGAATGACTGTGTGCTGTGCCCTGCCCAACAGGACA	408
QY	2772	GCAGTGGGAACCTAGCTACACTGAGCAGAGGAACCATGCGCTCCAGAGCTTGTATGCC	2831
Db	407	GCAGTGGGAACCTAGCTACACTGAGCAGAGGAACCATGCGCTCCAGAGCTTGTATGCC	348
QY	2832	ACTTGTATATATGAGATCAGAGAGATTAATATGCGAAAGTATATGATATGCTTAAG	2891
Db	347	ACTTGTATATATGAGATCAGAGAGATTAATATGCGAAAGTATATGATATGCTTAAG	288
QY	2892	ATTATATACAGTTGAAACCTGTAAATCTTCCCGAGAGGAGAAGGTTTCTGGAGCAGT	2951
Db	287	ATTATATACAGTTGAAACCTGTAAATCTTCCCGAGAGGAGAAGGTTTCTGGAGCAGT	228
QY	2952	GCAGTGGCAACAGCCACCATGTAAACCTCTGACCTGCCGTGCGTTCGGCTGTGGACA	3011
Db	227	GCAGTGGCAACAGCCACCATGTAAACCTCTGACCTGCCGTGCGTTCGGCTGTGGACA	168
QY	3012	GAGAGACATCAAGGTGAGAGGTGCGCTTCTGCGCTTCCTGTTAATTTGTAAATATTTGAGAA	3071
Db	167	GAGAGACATCAAGGTGAGAGGTGCGCTTCTGCGCTTCCTGTTAATTTGTAAATATTTGAGAA	108
QY	3072	GATTTATGTGACGACACACTTACAGAGCACAATGACAGTATATAGTCTGTGATATGAT	3131
Db	107	GATTTATGTGACGACACACTTACAGAGCACAATGACAGTATATAGTCTGTGATATGAT	48
QY	3132	AAATATATTCAAATATATGATATATATATATATATATATTTACAA	3175
Db	47	AAATATATTCAAATATATGATATATATATATATATATTTTAAAA	4
RESULT 3			
LOCUS	AU132307	803 bp	mRNA
DEFINITION	AU132307 NT2RP3 Homo sapiens cDNA clone NT2RP3004190 5', mRNA		
ACCESSION	AU132307		
VERSION	AU132307.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 803)		
	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,		
	Yamamoto, J., Wakamatsu, A., Nakamura, Y., Ngai, T., Sugano, S. and		
	Isogai, T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai		
	Genomics Laboratory		
	Helix Research Institute		
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
	Tel: 81-438-52-3975		
	Fax: 81-438-52-3986		
	Email: genomeshri.co.jp		
	HRI human cDNA project; 5' - & 3' - end one pass sequencing: Helix		
	Research Institute; cDNA library construction: Department of		
	Helix Research, Institute of Medical Science, University of Tokyo, and		
	Helix Research Institute.		
FEATURES	Location/Qualifiers		
SOURCE	1..803		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="NT2RP3004190"		

Query Match	Best Local Similarity	17.9%	Score 762.8	DB 9	Length 803
Matches 790	Conservative	0	Mismatches 10	Indels 3	Gaps 2
Query 1434	AATCGCCTATGTTGGTGAACAGTACCTCTGTGCGAATGAAGAACACGACCAAGAGCC	1493			
Db 1	AATCGCCTATGTTGGTGAACAGTACCTCTGTGCGAATGAAGAACACGACCAAGAGCC	60			
Query 1494	AGACTTCACAGCCAGCCGCTGTGCACAAAGTGAACCAAGTATCCCTCGGAGACA	1553			
Db 61	AGACTTCACAGCCAGCCGCTGTGCACAAAGTGAACCAAGTATCCCTCGGAGACA	120			
Query 1554	GGTAACAGTTTGGGCTGAGTCCAGCTCCCTCCTGAAATCAGAACACCCGCTGTGAGAT	1613			
Db 121	GGTAACAGTTTGGGCTGAGTCCAGCTCCCTCCTGAAATCAGAACACCCGCTGTGAGAT	180			
Query 1614	AACAAACAGCCCTCTCTTCAACAGGACAGACACCCCAATGCTGAGGAGGTTCCGAGATGA	1673			
Db 181	AACAAACAGCCCTCTCTTCAACAGGACAGACACCCCAATGCTGAGGAGGTTCCGAGATGA	240			
Query 1674	ACTTCCAGAGCAACCCAAATGGAGTTTCCAAAGATTAAGCTGACACTGGGAGACCCCT	1733			
Db 241	ACTTCCAGAGCAACCCAAATGGAGTTTCCAAAGATTAAGCTGACACTGGGAGACCCCT	300			
Query 1734	GGGAGAGGTTCTTTGGGCAAGTGGTCTATGGCGGAAGAGAGGGAATGACAAAGACAA	1793			
Db 301	GGGAGAGGTTCTTTGGGCAAGTGGTCTATGGCGGAAGAGAGGGAATGACAAAGACAA	360			
Query 1794	GGCCAAGAGGCGGTACCCGTGCGGTGAAGATGTTGAAAGATGATGCGCACAGAAAGA	1853			
Db 361	GGCCAAGAGGCGGTACCCGTGCGGTGAAGATGTTGAAAGATGATGCGCACAGAAAGA	420			
Query 1854	CCTTTCTGATCTGCTGTCAAGATGAGATGTAAGATGATGGGAAACACAGAATAT	1913			
Db 421	CCTTTCTGATCTGCTGTCAAGATGAGATGTAAGATGATGGGAAACACAGAATAT	480			
Query 1914	CATTAATCTCTTGGAGCTGACACAGAGATGGGCTCTATGTCATAGTTGATATAGC	1973			
Db 481	CATTAATCTCTTGGAGCTGACACAGAGATGGGCTCTATGTCATAGTTGATATAGC	540			
Query 1974	CTCTAAAGGCAACTCCGAAATACCTCCGAGACCCGAGAGCCACCCGGATGAGTACTC	2033			
Db 541	CTCTAAAGGCAACTCCGAGATACCTCCGAGACCCGAGAGCCACCCGGATGAGTACTC	600			
Query 2034	CTATGACATTAACCGTGTCTGTGAGAGACAGATGACCTTCAAGACCTTGGTCTGAC	2093			
Db 601	CTATGACATTAACCGTGTCTGTGAGAGACAGATGACCTTCAAGACCTTGGTCTGAC	660			
Query 2094	CTACGAGCTGGCGAGAGGATGAGTACTGGCTTCCCAAAAATATATCATCGAGATTT	2153			
Db 661	CTACGAGCTGGCGAGAGGATGAGTACTGGCTTCCCAAAAATATATCATCGAGATTT	719			
Query 2154	AGCAGCCAGAAATGTTTGGTAAACAGAAACAGTGTGATGAATAGCAGACTTT--GGA	2211			
Db 720	AGCAGCCAGAAATGTTTGGTAAACAGAAACAGTGTGATGAATAGCAGACTTT--GGA	779			
Query 2212	CTGCGCAGAGATATCAACAATAT 2234				
Db 780	TCGNCACAGAGATATCAACAATAT 802				

accession B0879891 clone IMAGE:6182720 5', mRNA sequence.
 version B0879891.1 GI:22271899
 keywords EST.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 reference 1 (bases 1 to 987)
 NIH-MGC http://mgc.nci.nih.gov/
 title National Institutes of Health, Mammalian Gene Collection (MGC)
 journal Unpublished (1999)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 plate: L1AM13569 row: c column: 09
 high quality sequence stop: 645.
 features
 source
 1..987
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6182720"
 /clone_lib="Lupski_dorsal_root_ganglion"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGGCTCG-3' and
 5'-GACTAGTTCATGCGCGAGCGCGCCCT(15)-3', size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
 BASE COUNT 300 a 203 c 180 g 304 t
 ORIGIN
 Query Match 17.1%; Score 731.4; DB 14; Length 987;
 Best Local Similarity 94.5%; Pred. No. 1.3e-144;
 Matches 791; Conservative 0; Mismatches 41; Indels 5; Gaps 3;
 Oy 2580 CTGGACCTCAGCAACCTCTGACAGATATTCACCTAGTACCTGACACAAGATTG 2639
 |||||||
 Db 11 CTGGACCTCAGCAACCTCTGACAGATATTCACCTAGTACCTGACACAAGATTG 70
 Oy 2640 TTGCTCTTCAGAGATGATGTTGTTTTTCTCCAGACCCCATGCTTACGAACATGCT 2699
 |||||||
 Db 71 TTGCTCTTCAGAGATGATGTTGTTTTTCTCCAGACCCCATGCTTACGAACATGCT 130
 Oy 2700 TCTCTGATTCACACATATAAGGCGAGTGTAAACATGAATGATGCTGCTGCTGCTC 2759
 |||||||
 Db 131 TCTCTGATTCACACATATAAGGCGAGTGTAAACATGAATGATGCTGCTGCTGCTC 190
 Oy 2760 CCNAACGAGACGACCTGGGAACCTAGCTACACTGAGCAGGAGACCATGCTCCAGAG 2819
 |||||||
 Db 191 CCNAACGAGACGACCTGGGAACCTAGCTACACTGAGCAGGAGACCATGCTCCAGAG 250
 Oy 2820 CTGTTGTCCTCACTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2879
 |||||||
 Db 251 CTGTTGTCCTCACTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 310
 Oy 2880 ATATGCTGAAGATTTATACAGTGAAGAACTGTATATCTTCCACAGACAGAGAAGGT 2939
 |||||||
 Db 311 ATATGCTGAAGATTTATACAGTGAAGAACTGTATATCTTCCACAGACAGAGAAGGT 370

Oy 2940 TTCTGGACAGCTGGACCTGCCACAAGCCACCATGTAAACCCCTTCACCTGCCGTCCTT 2999
 |||||||
 Db 371 TTCTGGACAGCTGGACCTGCCACAAGCCACCATGTAAACCCCTTCACCTGCCGTCCTT 430
 Oy 3000 GCGTGTGACAGTACAGCTCAAGGTGAGCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 3059
 |||||||
 Db 431 GCGTGTGACAGTACAGCTCAAGGTGAGCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 490
 Oy 3060 ATAAATGAGAAATTTATGTCACACACACTTACAGAGCACAATACAGTATATAGTG 3119
 |||||||
 Db 491 ATAAATGAGAAATTTATGTCACACACACTTACAGAGCACAATACAGTATATAGTG 550
 Oy 3120 CTGATGATGATTAATATATTTCAATATGTAATAATATATATATATATATATATATAT 3179
 |||||||
 Db 551 CTGATGATGATTAATATATTTCAATATGTAATAATATATATATATATATATATATAT 610
 Oy 3180 TTATTTTGTATGATTTTAAATGATGATGCCAATGACCTAG-AAAATGGTCTGCT 3238
 |||||||
 Db 611 TTATTTTGTATGATTTTAAATGATGATGCCAATGACCTAGAAAATGGTCTGCT 670
 Oy 3239 TTTTAAATGATGATTTGCTAAATGCTGCTCTTACACATATTTCTTAATTTGACCGAG 3298
 |||||||
 Db 671 TTTTAAATGATGATTTGCTAAATGCTGCTCTTACACATATTTCTTAATTTGACCGAG 730
 Oy 3299 CAGAGTGGAATAATATCTTTT---GCTTCAGGGAATAATGATATACGT-TAATTTATTA 3354
 |||||||
 Db 731 CAGAGTGGAATAATATCTTTTGGCTTCACGGAATAATGATATACGTCAATTTATTA 790
 Oy 3355 ATAAATGCTATATATACAAACATTAATATCAATTTTATTTTGTGTAATTAAGT 3411
 |||||||
 Db 791 ATAAATGCTATATATATACAAACATTAATATCAATTTTATTTTGTG 847
 RESULT 5
 LOCUS B6598600 834 bp mRNA linear EST 02-MAY-2001
 DEFINITION B6598600
 mRNA sequence.
 accession B6598600
 version B6598600.1 GI:13966051
 keywords EST.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 reference 1 (bases 1 to 834)
 NIH-MGC http://mgc.nci.nih.gov/
 title National Institutes of Health, Mammalian Gene Collection (MGC)
 journal Unpublished (1999)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
 Sequencing by: Incey Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 plate: L1AM10694 row: 1 column: 16
 high quality sequence start: 7
 high quality sequence stop: 833.
 features
 source
 1..834
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4801623"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

Db 323 AATTGAACACAGAGTTGCTTCTGATAGTGTGGGAGTACGTCATCTTTTAAAGGA 264
Oy 3969 TTGCTTCATCTAATTTGGCAGACCTACCAAAAAGATCCAGCTCATACATACAG 4028
Db 263 TTGCTTATCTAATTTGGCAGACCTACCAAAAAGATCCAGCTCATACATACAG 204
Oy 4029 ACAAATATGCGCCGTTGTTCTCTGTACTAAAGTATGTTTTGCTTGGAAACACC 4088
Db 203 ACAAATATGCGCCGTTGTTCTCTGTACTAAAGTATGTTTTGCTTGGAAACACC 144
Oy 4089 ACTGCTTTCGCAATGCGCTGCAAGATGACATGACATGATCTTATGTGTACAA 4148
Db 143 ACTGCTTTCGCAATGCGCTGCAAGATGACATGATGATCTTATGTGTACAA 84
Oy 4149 AATTGAGAAAGTATTTATATAAACCTGTTAATTTTACTGACAAATAAATGTTCT 4208
Db 83 AATTGAGAAAGTATTTATATAAACCTGTTAATTTTACTGACAAATAAATGTTCT 24
Oy 4209 ACAGATATTATGTTTACAGACAG 4231
Db 23 ACAGATATTATGTTTACAGACAG 1

RESULT 7
A1436212/c 755 bp mRNA linear EST 13-APR-1999
LOCUS A1436212
DEFINITION UH8905.x1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:2124824
3', similar to gb:M87770 FIBROBLAST GROWTH FACTOR RECEPTOR 2
PRECUSOR (HUMAN);, mRNA sequence.
A1436212
VERSION A1436212.1 GI:4308606
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 755)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgarbs-remail.nih.gov
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert length: 895 Std Error: 0.00
Seq primer: -409P from Glbco
High quality sequence stop: 443.
Location/Qualifiers
1. 755
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2124824"
/clone_1lb="Soares_NHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pTT3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHn, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 252 a 139 c 147 g 216 t 1 others
ORIGIN

Query Match 16.1%; Score 686.8; DB 9; Length 755;
Best Local Similarity 96.0%; Pred. No. 3.7e-135;

Matches 725; Conservative 0; Mismatches 28; Indels 2; Gaps 2;
Oy 3439 ACTAGTATATCTATGCTTGAGACTAATCTAGTTATACAGATCTTTGAAGAAGATATTT 3498
Db 755 ACTAGTATATCTATGCTTGAGACTAATCTAGTTATACAGATCTTTGAAGAAGATATTT 696
Oy 3499 ACAATATATGACTAATTTTGGGAAAATGAAAGTTTGATTTATTTGCTTTTAAATGCTCT 3558
Db 695 ACAATATATGACTAATTTTGGGAAAATGAAAGTTTGATTTATTTGTTAAATGCTGCT 636
Oy 3559 GTGACAGCATTTGTTTGAAGCTCTCTAAATGCCCATTTTAAAGACTATCTATAGA 3618
Db 635 GTCAACACANTGTTCTTGAAGCTCTCTAAATGCCCATTTTAAAGACTATCTATAGA 576
Oy 3619 AGGTGTTTCATTTTGGTGTGACACCTGTCATTAAGTCAAGCAACGCTAAGTGAAGTT 3678
Db 575 AGGTGTTTCATTTTGGTGTGACACCTGTCATTAAGTCAAGCAACGCTAAGTGAAGTT 516
Oy 3679 CCCAAGATTAATGATGACAGGCTCTCTTAAAGATGCTTAAATCCATTCCTTGAGACA 3738
Db 515 CCCAAGATTAATGATGACAGGCTCTCTTAAAGATGCTTAAATCCATTCCTTGAGACA 456
Oy 3739 GACCTTATGTAATGATAGCAAGATGCTTCTCTGCGACGCTGACCTTCTGCTTG 3798
Db 455 GACCTTATGTAATGATAGCAAGATGCTTCTCTGCGACGCTGACCTTCTGCTTG 396
Oy 3799 AGTTCACATTAATGATAGATGACCTG-ATTCCTTCAGTGAATTTGATAGGCTTCCA 3857
Db 395 AGTTCACATTAATGATAGATGACCTGATTTCTCTCAGTGAATTTGATAGGCTTCCA 336
Oy 3858 GACTCTTT-GCGTTGAGACAGCGCTGTTAGATCTTCAAGTCCCATATAGAAATTTGAA 3916
Db 335 GACTCTTTGGCGTTGAGACAGCGCTGTTAGATCTTCAAGTCCCATATAGAAATTTGAA 276
Oy 3917 CACAGAGTTGTTCTGCTATAGTATTTGGGATAGCTCCATCTTTTAAAGATGCTTTC 3976
Db 275 CACAGAGTTGTTCTGCTATAGTATTTGGGATAGCTCCATCTTTTAAAGATGCTTTC 216
Oy 3977 ATCTAATCTGGCAGACCTCACCAAAAGATCCACCTCATACCTACATGACAAATA 4036
Db 215 ATCTAATCTGGCAGACCTCACCAAAAGATCCACCTCATACCTACATGACAAATA 156
Oy 4037 TCGCGTGTTCCTCTCTACTAAAGTATGTTTGGCTTGGAAACACCACCTCACTT 4096
Db 155 TCGCGTGTTCCTCTCTACTAAAGTATGTTTGGCTTGGAAACACCACCTCACTT 96
Oy 4097 TGCATATACCGCGTGAAGATGAATGACATGATCTTATGTGTACAAATTTGGAG 4156
Db 95 TGCATATACCGCGTGAAGATGAATGACATGATCTTATGTGTACAAATTTGGAG 36
Oy 4157 AAAGTATTATTAATAAACCTGTTAATTTTATACCTG 4191
Db 35 AAAGTATTATTAATAAACCTGTTAATTTTATACCTG 1

RESULT 8
BM792391 693 bp mRNA linear EST 05-MAR-2002
LOCUS BM792391
DEFINITION K-EST0072606 S22SN016n1 Homo sapiens cDNA clone S22SN016n1-28-B10
5', mRNA sequence.
ACCESSION BM792391
VERSION BM792391.1 GI:19140623
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 693)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-gong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemil.kr@kribb.re.kr
Plate: 28 row: B column: 10
High quality sequence stop: 693.
Location/Qualifiers
1. 693

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-28-B10"
/clone_lib="S22SNU16n1"
/sex="F"
/tissue_type="ascites"
/cell_type="lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT73-Pac; Site: 1: EcoRI; Site: 2: NotI; The S22SNU16 library was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

BASE COUNT 191 a 177 c 189 g 136 t

ORIGIN

Query Match 15.9%; Score 680.4; DB 14; Length 693;
Best Local Similarity 99.9%; Pred. No. 8.6e-134;
Matches 681; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1454 CAGTCATCTCTGCGGATGGAAGACAGACCAAGCCAGACTTCACAGCCAGCCGG 1513
DB 1 CAGTCATCTCTGCGGATGGAAGACAGACCAAGCCAGACTTCACAGCCAGCCGG 60
QY 1514 CTGTGCACAGCTGACCAACGATCCCTCGGAGACAGGTAACGTTTGGGCTGACT 1573
DB 61 CTGTGCACAGCTGACCAACGATCCCTCGGAGACAGGTAACGTTTGGGCTGACT 120
QY 1574 CCAGCTCTCATGTAAGTCCAAACCCCGCTGGTAGTAACAACACGCTCTTTCAA 1633
DB 121 CCAGCTCTCATGTAAGTCCAAACCCCGCTGGTAGTAACAACACGCTCTTTCAA 180
QY 1634 CGGACAGACACCCCATGCTGGGAGGGGTCTCGAGTATGACTTCCAGAGACCCAAAT 1693
DB 181 CGGAGACACCCCATGCTGGGAGGGGTCTCGAGTATGACTTCCAGAGACCCAAAT 240
QY 1694 GGGAGTTTCCAGAGTAAGTGTGACACTGGGCAAGCCCTGGAGAGAAAGTTGCTTGGGC 1753
DB 241 GGGAGTTTCCAGAGTAAGTGTGACACTGGGCAAGCCCTGGGAGAGAAAGTTGCTTGGGC 300
QY 1754 AAGTGTCTATGGCGGAAGAGTGGGAATTGACAAAGCCCAAGGAGGCGGTACCG 1813
DB 301 AAGTGTCTATGGCGGAAGAGTGGGAATTGACAAAGCCCAAGGAGGCGGTACCG 360
QY 1814 TGGCCGTGAAGATGTTGAAGATGATCCACAGAGAAAACCTTTCTGATGCTGTGACG 1873
DB 361 TGGCCGTGAAGATGTTGAAGATGATCCACAGAGAAAACCTTTCTGATGCTGTGACG 420
QY 1874 AGATGAGATGATGAAGATGATTTGGAAACACAGAATATCAATATCTTTGGAGCCT 1933
DB 421 AGATGAGATGATGAAGATGATTTGGAAACACAGAATATCAATATCTTTGGAGCCT 480
QY 1934 GCACACAGATGGGCTCTCTATGTCATAGTTAGTATGCTCTAAAGGCAACCTCCGAG 1993
DB 481 GCACACAGATGGGCTCTCTATGTCATAGTTAGTATGCTCTAAAGGCAACCTCCGAG 540
QY 1994 AATACCTCGAGCCCGGAGGCCACCGGGATGAGTACTCCATATGACATTAAACCGTTC 2053

DB 541 AATACCTCGAGCCCGGAGGCCACCGGGATGAGTACTCCATATGACATTAAACCGTTC 600
QY 2054 CTGAGAGCAGATGACTTCAAGACTTGTGTGATGACACCTACAGCTGGCCAGAGCA 2113
DB 601 CTGAGAGCAGATGACTTCAAGACTTGTGTGATGACACCTACAGCTGGCCAGAGCA 660
QY 2114 TGGAGTACTTGGCTCCCAAA 2135
DB 661 TGGAGTACTTGGCTCCCAAA 682

RESULT 9
AI433805/c
LOCUS
DEFINITION
AI433805 822 bp mRNA linear EST 30-MAR-1999
th81f11.x1 Soares.NHMPu-S1 Homo sapiens cDNA clone IMAGE:2125101
3' similar to gb:U87770 FIBROBLAST GROWTH FACTOR RECEPTOR 2
PRECURSOR (HUMAN); mRNA sequence.
AI433805
VERSION
KEYWORDS
AI433805.1 GI:4291750
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 822)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1043 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 436.
Location/Qualifiers
1. 822

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2125101"
/clone_lib="Soares.NHMPu-S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2bBM, pregnant uterus NBHPu, and fetal heart NBH19M) were mixed, and ss circles were made in vitro. Following MAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 248 a 153 c 161 g 260 t

ORIGIN

Query Match 15.8%; Score 675.6; DB 9; Length 822;
Best Local Similarity 93.9%; Pred. No. 8.7e-133;
Matches 759; Conservative 0; Mismatches 39; Indels 10; Gaps 5;

QY 3463 TAACATGTTATGATGATCCCTTTGAAAGAAATTTTACAATATGACTTAATTTGGGAA 3522
DB 811 TAACATGTTATGATGATCCCTTTGAAAGAAATTTTACAATATGAGCTA----TTGGGGA 757
QY 3523 AATGAATTTGATTTATTTGTTTAAATGCTGCTGACAGATGTTCTTAAAGCTC 3582
DB 756 AAAAGAGTTTGAATTTATTTTGGTTAAAGGCGCGCTGACGGA--TGGTTCTAGCCCTC 699
QY 3583 CTAAATGCCCATATTTAAAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAAC 3642

```

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 698 CTAAGACCCCAATATTTAAA-AACTCATTCATAGGAAGGTGTTCCATTTGGGTGTCAC 640
Qy 3643 CCTGTCATTCAGTCACGACGAACGTCTAACTGACATTCCTCCAAATAAATGTTACAGCCT 3702
Db 639 CCGTCATTCAGTCACGACGAACGTCTAACTGACATTCCTCCAAATAAATGTTACAGCCT 580
Qy 3703 CTTTAAAGATGCTTAAATGACATTCCTGAGACAGACCTTAAATGAAATATAGACAGA 3762
Db 579 CTTTAAAGATGCTTAAATGACATTCCTGAGACAGACCTTAAATGAAATATAGACAGA 520
Qy 3763 AATGCTTCTCTGAGACAGCTGCTTCTGCTTCTGAGTTGACATTAATGACATTAAGCC 3822
Db 519 AATGCTTCTCTGAGACAGCTGCTTCTGCTTCTGAGTTGACATTAATGACATTAAGCC 460
Qy 3823 TG-ATTCTCTTCAAGTAATTTGATTAATGCTTCCAGACTCTTT-GCGTTGAGACGCT 3880
Db 459 TGTATCTCTTCAAGTAATTTGATTAATGCTTCCAGACTCTTTGCGCTTGGAGACGCT 400
Qy 3881 GTTAGCATCTTCAGTCCCATCATAGAAAATTGAAACACAGAGTTGCTGCTGATAGTT 3940
Db 399 GTTAGCATCTTCAGTCCCATCATAGAAAATTGAAACACAGAGTTGCTGCTGATAGTT 340
Qy 3941 TTGGGATACGTCATCTTTTAAAGGATTCCTTCAATCTAATCTGAGACAGCTCACC 4000
Db 339 TTGGGATACGTCATCTTTTAAAGGATTCCTTCAATCTAATCTGAGACAGCTCACC 280
Qy 4001 AAAAGATCAGGCTCTACTACTACATACAGCAAAATATGCGCGTGTCTCTGTACTAA 4060
Db 279 AAAAGATCAGGCTCTACTACTACATACAGCAAAATATGCGCGTGTCTCTGTACTAA 220
Qy 4061 AGTATGCTTTTGTGTTGGAACACCCAGCTGCTTGCATAGCCGTGCAAGATGATG 4120
Db 219 AGTATGCTTTTGTGTTGGAACACCCAGCTGCTTGCATAGCCGTGCAAGATGATG 160
Qy 4121 CAGATTACACGTATCTTATGCTTACAAAATTGAGAAAGTATTAATAAAACCTGTAA 4180
Db 159 CAGATTACACGTATCTTATGCTTACAAAATTGAGAAAGTATTAATAAAACCTGTAA 100
Qy 4181 TTTTCTACTGACAAATAAATGTTCTACAGATTAATTAATTAACAACAATAAAT 4240
Db 99 TTTTCTACTGACAAATAAATGTTCTACAGATTAATTAATTAACAACAATAAAT 40
Qy 4241 GTACGCACTTAAAAAATGTTCTACAGATTAATTAATTAACAACAATAAAT 4268
Db 39 GTACGCACTTAAAAAATGTTCTACAGATTAATTAATTAACAACAATAAAT 12

RESULT 10
BM970064/C 690 bp mRNA linear EST 21-MAR-2002
LOCUS 1 UI-CF-EC1-abu-b-07-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
DEFINITION UI-CF-EC1-abu-b-07-0-UI 3', mRNA sequence.
ACCESSION BM970064
VERSION BM970064.1 GI:19587651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 690)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtracction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu

```

```

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT, rich#low complexity (matched complement)
216-266, >(TA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
location/Qualifiers
1..690
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-abu-b-07-0-UI"
/clone_11b="UI-CF-EC1"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal Lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGTGGCTTAC.
TAG_L1B=UI-CF-EC1
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_SEQ=AGTGGCTTAC"

BASE COUNT 210 a 136 c 120 g 224 t
ORIGIN

Query Match 15.8%; Score 675; DB 14; Length 690;
Best Local Similarity 99.3%; Pred. No. 1.2e-133;
Matches 678; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2700 TCCTCAGTATCCACATTAACGCGCAGTGTAAACATGAATGACTGTCTGCTGCTCC 2759
Db 690 TCCTCAGTATCCACATTAACGCGCAGTGTAAACATGAATGACTGTCTGCTGCTCC 631
Qy 2760 CCAACAGCAGCAGCAGTGGAACTAGCTACACTGACGGGAGACCAATGCCCGCAGAG 2819
Db 630 CCAACAGCAGCAGCAGTGGAACTAGCTACACTGACGGGAGACCAATGCCCGCAGAG 571
Qy 2820 CTTGTTGCTCCACTGTATATGATGATCAGAGGATTAATTAATGAAAGTAACTACAC 2879
Db 570 CTTGTTGCTCCACTGTATATGATGATCAGAGGATTAATTAATGAAAGTAACTACAC 511
Qy 2880 AATATGTAAGATTTATACAGTTGAAAACCTGTAACTTCCCGAGAGACAGAGGT 2939
Db 510 AATATGTAAGATTTATACAGTTGAAAACCTGTAACTTCCCGAGAGACAGAGGT 451
Qy 2940 TTCTGAGCAGTGGACTGGCACAAGCCACATGTAAACCCCTCAGCTGCGCTGCTCT 2999
Db 450 TTCTGAGCAGTGGACTGGCACAAGCCACATGTAAACCCCTCAGCTGCGCTGCTCT 391
Qy 3000 GCGTGGACAGTGAAGACTCAAGGTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 3059
Db 390 GCGTGGACAGTGAAGACTCAAGGTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 331
Qy 3060 AATAATTGAGAAATTTATGTCAGCAGACACTTTACAGAGACAAATGAGATTAATAGTG 3119
Db 330 AATAATTGAGAAATTTATGTCAGCAGACACTTTACAGAGACAAATGAGATTAATAGTG 271

```


FEATURES
SOURCE

```

location/Qualifiers
1. 693
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="U1-H-E21-bbh-9-11-0-01"
/clone_1b="NCI_CGAP_Ch2"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Left pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I
Following ligation: Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GATCAGCGCT."

```

BASE COUNT	212 a	135 c	123 g	223 t
ORIGIN				

Query Match	15.68;	Score 666;	DB 14;	Length 693;
Best Local Similarity	99.18;	Pred. NO. 9.7e-131;		
Matches 680; Conservative	0;	Mismatches 5;	Indels 1;	Gaps 1;

QY	2698	CTTCCAGATATCCACACATTAACGGCAGGTTAAACATGTAATGCTGTCTCCGCT	2757
Dp	693	CTTCTCAGTATCCACACATTAACGGCAGTGTAAACATGTAATGCTGTCTCCGCT	634
QY	2758	CCCCAAACAGACAGCAGCTGGGAACCTACTACACAGACAGGAGACATGCTCCGAG	2817
Dp	633	CCCCAAACAGACAGCAGCTGGGAACCTAGTAGTACAGACAGGAGAGACATGCTCCGAG	574
QY	2818	AGCTTGTGTCGCACCTTGTATATATGATCAGAGAGATAAATTAATTGGAAAAGTATCA	2877
Dp	573	AGCTTGTGTCGCACCTTGTATATATGATCAGAGAGATAAATTAATTGGAAAAGTATCA	514
QY	2878	GCATATGTGAAAGATTTATACGTTGAAACCTGTAACTTCCCAGAGAGAGAAAGAG	2937
Dp	513	GCATATGTGAAAGATTTATACGTTGAAACCTGTAACTTCCCAGAGAGAGAAAGAG	454
QY	2938	GTTTCTTGAGCAGCTGACATGCCCAAGGCCACCATGTAAACCCCTCAGCTGGCGCTT	2997
Dp	453	GTTTCTTGAGCAGCTGAGCATGCCCAAGGCCACCATGTAAACCCCTCAGCTGGCGCTA	394
QY	2998	CTGGCTGTGACACAGTACAGCATCAAGGTGAGCTGCGTTCTGCTTTCCTGTAAATTTTG	3057
Dp	393	TTCGCTGTGACACAGTACAGCATCAAGGTGAGCTGCGTTCTGCTTTCCTGTAAATTTTG	334
QY	3058	TAAATTAATGGAGAAGTTTATGTGCACACACACCTTAACAGAGCAAAATGACATATATAG	3117
Dp	333	TAAATTAATGGAGAAGTTTATGTGCACACACACCTTAACAGAGCAAAATGACATATATAG	274
QY	3118	TGCTGATGTATCTAAATATATATTCGAAATATATGATATAAATATATATATATATTCAGAG	3177
Dp	273	TGCTGATGTATCTAAATATATATTCGAAATATATGATATAAATATATATATATATTCAGAG	214
QY	3178	AGTTATTTTGTATGTATTTAAATGATGTGCCAATGCACCTAGAAAATTTGCTCTC	3237
Dp	213	AGTTATTTTGTATGTATTTAAATGATGTGCCAATGCACCTAGAAAATTTGCTCTC	154
QY	3238	TTTTTTTAAATAGCTATTTGCTAAATGCTGTCTGTACACATAATTTCTTAATTTTACCGA	3297
Dp	153	TTTTTTTAAATAGCTATTTGCTAAATGCTGTCTGTACACATAATTTCTTAATTTTACCGA	94

[illegible]

RESULT	13
LOCUS	B1661597
DEFINITION	B1661597 850 bp mRNA linear EST 12-SEP-2000 6033055723r1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5315197 5'
ACCESSION	B1661597
VERSION	B1661597.1 GI:15575833
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 850)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1998)
COMMENT	Contact: Robert Strausberg, Ph.D.

Yr	Accession	Sequence	Score	DB	Length	Gaps
0y	1340	GCTTGACAGTTCGCGCCGCCCTG-GAAGAGAAAGAGATTACAGCTCCCGAGACTAC	15.6%	DB 13	850	5
Db	1	GGTTGACAGTTCTCGCCAGCGCTGTATGAGGAGGAAGATACAGCGCTCCCGAGATTAT	Best Local Similarity 90.1%; Pred. No. 1.9e-130;			
		Matches 767; Conservative 0; Mismatches 79; Indels 5; Gaps 5				
0y	1399	CTGGAGATAGCATTTACTGCGATAGGGGCTCTTAATCGCTGTATGGGTAAACAGTC			1458	
Db	61	CTGGAGATAGCATTTACTGCGATAGGGGCTCTTAATCGCTGTATGGGTAAACAGTC			120	
0y	1459	ATTCGTGCGGAAATAGAACACAGCAAGAAAGAGCAGACTTCA-GCAGCCAGCGGCTGT			1517	
Db	121	ATCTTTTGGCGAATAAAGCCAGCAAGCAAGAACGCAAGCTTCAAGCAGCAGCCAGCTGT			180	
0y	1518	GCACAGCTGACCAACGATTATCCCTCGCGAGACAGAGTAAACAGTTTCGGCTGAGTCCAG			1577	

```
||||| 181 GCACAGGCTGACCAAGCCGATCCCTCGGAGACAGTACAGTTCCGCCGAGTCCAG 240
||||| 1578 CTCCTCCATGAATCTCAACACCCCGTGTGAGATTAACACAGCCCTCTCTCAACGCC 1637
||||| 241 CTCCTCCATGAATCTCAACACCCCGTGTGAGATTAACACAGCCCTCTCTCAACACC 300
||||| 1638 AGACACCCCATGCTGGCAGAGGGGTCTCCAGATATGAACCTCCAGAGAGACCCCAAAATGGGA 1697
||||| 301 GGACACCCCATGCTGGCAGAGGGGTCTCCAGATATGAATGATGCCAAGAGATCCAAAGTGGGA 360
||||| 1698 GTTCCAGAGATTAAGCTGACACTGGCCAGCCCTCGGAGAGAGTGTCTTTGGCACT 1757
||||| 361 ATTCCCATGAGATTAAGCTGACACTGGCCAGCCCTCGGAGAGAGTGTCTTTGGCACT 420
||||| 1758 GGTACGGGCGGAGAGAGTGGGAATTGACAAAGACAAAGCCAGAGGCGGTCAACCGTGC 1817
||||| 421 AGTCATGCTGTAAGAGATGGGATGATTAAGACAAACCAAGAGGCGGTCAACCGTGC 480
||||| 1818 CGTGAAGATGTTGAA-AGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTACAGAGA 1876
||||| 481 AGTGAAGATGTTGAA-AGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTACAGAGA 540
||||| 1877 TGGAGATGATGAAGATGATGGGAAACACAGAAATATCAATCTTCTTGGAGCCTGCA 1936
||||| 541 TGGAGATGATGAAGATGATGGGAAACATMAACATTAATCAACCTCTCTGCGGCGCTGCA 600
||||| 1937 CACAGAGTGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1996
||||| 601 CCGAGAGATGAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
||||| 1997 ACCCTCGAGCCCGGAGAGCCCGGAGATGATGATGATGATGATGATGATGATGATGATGAT 2055
||||| 661 ACCCTCGAGCCCGGAGAGCCCGGAGATGATGATGATGATGATGATGATGATGATGATGAT 719
||||| 2056 GAGGAGCAGATACCTTCAAGACCTTGTGATGATGATGATGATGATGATGATGATGATGATG 2115
||||| 720 GAGGAGCAGATACCTTCAAGACCTTGTGATGATGATGATGATGATGATGATGATGATGATG 779
||||| 2116 GAGTACTGCTGCTCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2175
||||| 780 GAGTACTGCTGCTCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 839
||||| 2176 ACAGAAACAA 2186
||||| 840 ACAGAAACAA 850

RESULT 14
LOCUS B161662 787 bp mRNA linear EST 12-SEP-2001
DEFINITION 603305601P1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5351304 5',
ACCESSION B161662.1
VERSION B161662.1 GI:15575898
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 787)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgep@b-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furch
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
```

```
http://image.llnl.gov
Plate: LLML1893 row: a column: 01
High quality sequence stop: 787.
FEATURES
source
1. 787
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5351304"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-Sport6; Site: 1; SalI;
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furch,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
```

BASE COUNT 223 a 176 c 221 g 167 t

ORIGIN

Query Match 15.6% Score 664; DB 13; Length 787;
Best Local Similarity 91.0%; Pred. No. 2.5e-130;
Matches 717; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

```
QY 1665 CGAGTATGACTTCCAGAGACCCAAATGGAGTTTCCAAAGATTAAGCTACACTGGG 1724
||||| 1 CGAGTATGAGTTGCCAGAGATCCAAAGTGGAGATTTCCCAAGATTAACCTACCTGGG 60
DB 1725 CAAGCCCTGGGAGAAAGTGTGCTTGGGCAAGTGGTCAATGGGAGAGAGTGAATTGA 1784
||||| 61 CAACCCCTGGGAGAAAGTGTGCTTGGGCAAGTGGTCAATGGTCAATGGTGAATGCA 120
QY 1785 CAAAGCAAGCCCAAGAGAGCGGTCAACCGTGGCCGTGAAGATGTTGAAGATATGCCAC 1844
||||| 121 TAAAGCAAAACCAAGAGAGCGGTCAACCGTGGCAGAGATGTTGAAGATATGCCAC 180
DB 1845 AGAGAAAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1904
||||| 181 AGAGAAAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 1905 CAAGAATATCATTAATCTTCTTGGAGCCCTGCACACAGATGAGGCTCTGATGATGAT 1964
||||| 241 TAAAGCAATTAACACTCTCTGGGCGCTGCACAGAGATGATGATGATGATGATGATGAT 300
DB 1965 TGAGTATGCTCTTAAAGCAACCTCCGAGATACCTCCGAGCCCGAGGCCACCCGGAT 2024
||||| 301 TGAATATGATGAGAAAGCAACCTCCGAGATACCTCCGAGCCCGAGGCCACCTGGCAT 360
QY 2025 GGAGTACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2084
||||| 361 GGAGTACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 2085 GTTATGACACTTACAGAGCTGGCCAGAGGAGATGAGTACTGCTTCCCAAAATGATTTCA 2144
||||| 421 GTTATGACACTTACAGAGCTGGCCAGAGGAGATGAGTACTGCTTCCCAAAATGATTTCA 480
DB 2145 TCGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACAAATGATGATGATGATGATGAT 2204
||||| 481 TCGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACAAATGATGATGATGATGATGAT 540
QY 2205 GTTGGAGCTGGCCAGAGATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAAT 2264
||||| 541 GTTGGAGCTGGCCAGAGATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAAT 600
DB 2265 GCTTCCAGTCAAGTGAATGCTTCCAGAAAGCCCTGTTGATAGTATACACTCATCAGAG 2324
||||| 601 ACTTCCAGTCAAGTGAATGCTTCCAGAAAGCCCTGTTGATAGTATACACTCATCAGAG 660
QY 2325 TGAATGCTGCTCTTGGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2384
||||| 661 CGATGCTGCTCTTGGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:40:42 ; Search time 120 seconds
(without alignments)
13868.608 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 ccacaagaccacactctctcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 segs, 194966369 residues

Total number of hits satisfying chosen parameters: 188974

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.2	0.6	31	10 US-09-801-274-958	Sequence 958, Appl
2	23.4	0.5	46	10 US-09-827-289-25	Sequence 25, Appl
3	22.6	0.5	31	10 US-09-801-274-957	Sequence 957, Appl
4	22.6	0.5	50	10 US-09-815-343-1012	Sequence 1012, Ap
5	22.4	0.5	46	10 US-09-827-289-21	Sequence 21, Appl
6	22	0.5	46	10 US-09-827-289-22	Sequence 22, Appl
7	21.8	0.5	44	10 US-09-875-519A-13	Sequence 13, Appl
8	21.8	0.5	46	10 US-09-827-289-24	Sequence 24, Appl
9	21.8	0.5	48	9 US-09-864-785-3604	Sequence 3604, Ap
10	21.6	0.5	46	10 US-09-827-289-26	Sequence 26, Appl
11	21.4	0.5	46	10 US-09-827-289-20	Sequence 20, Appl
12	21.4	0.5	35	9 US-09-827-289-24	Sequence 24, Appl
13	21.2	0.5	35	9 US-09-927-777A-72	Sequence 72, Appl
14	20.8	0.5	42	10 US-09-828-592-2	Sequence 2, Appl
15	20.8	0.5	46	10 US-09-827-289-20	Sequence 20, Appl
16	20.8	0.5	45	10 US-09-827-289-20	Sequence 30, Appl
17	20.6	0.5	45	10 US-09-967-055-30	Sequence 30, Appl
18	20.6	0.5	45	12 US-10-023-529-30	Sequence 30, Appl
19	20.6	0.5	45	12 US-10-023-523-30	Sequence 30, Appl

20	20.6	0.5	48	9 US-09-864-785-3333	Sequence 3333, Ap
21	20.6	0.5	48	9 US-09-864-785-3472	Sequence 3472, Ap
22	20.6	0.5	48	9 US-09-864-785-3501	Sequence 3501, Ap
23	20.2	0.5	32	10 US-09-465-802-32	Sequence 32, Appl
24	20.2	0.5	35	9 US-09-880-887-19	Sequence 19, Appl
25	20.2	0.5	37	9 US-09-996-634-144	Sequence 144, App
26	20.2	0.5	48	9 US-09-864-785-3578	Sequence 3578, Ap
27	20.2	0.5	48	10 US-09-732-914-68	Sequence 68, Appl
28	20.2	0.5	48	10 US-09-732-914-73	Sequence 73, Appl
29	20.2	0.5	48	10 US-09-732-914-80	Sequence 80, Appl
30	20	0.5	20	10 US-09-073-881-4	Sequence 4, Appl1
31	20	0.5	22	10 US-09-073-881-24	Sequence 24, Appl1
32	20	0.5	22	10 US-09-073-881-26	Sequence 26, Appl1
33	19.8	0.5	40	10 US-09-245-802-45	Sequence 45, Appl1
34	19.8	0.5	45	10 US-09-827-289-12	Sequence 12, Appl1
35	19.8	0.5	45	10 US-09-827-289-16	Sequence 16, Appl1
36	19.8	0.5	46	10 US-09-827-289-21	Sequence 21, Appl1
37	19.8	0.5	46	10 US-09-827-289-25	Sequence 25, Appl1
38	19.8	0.5	48	9 US-09-864-785-3109	Sequence 3109, Ap
39	19.8	0.5	48	9 US-09-864-785-3338	Sequence 3338, Ap
40	19.8	0.5	48	9 US-09-864-785-3425	Sequence 3425, Ap
41	19.8	0.5	48	9 US-09-864-785-3435	Sequence 3435, Ap
42	19.6	0.5	35	9 US-10-034-451-1	Sequence 1, Appl1
43	19.6	0.5	36	9 US-09-950-933A-99	Sequence 99, Appl1
44	19.6	0.5	36	9 US-10-047-593-6	Sequence 6, Appl1
45	19.6	0.5	36	9 US-10-090-035-25	Sequence 25, Appl1

ALIGNMENTS

RESULT 1
US-09-801-274-958
Sequence 958, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 958
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-958
Query Match 0.6%; Score 24.2; DB 10; Length 31;
Best Local Similarity 83.9%; Pred. No. 7.8e+03;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1034 ACCGCCCATCTCCAGCCGACGCGCGC 1064
DB 1 ACCGCCCATCTCGRGGCGGCGCGCGC 31
RESULT 2
US-09-827-289-25/c
Sequence 25, Application US/09827289
Patent No. US20020009716A1
GENERAL INFORMATION:
APPLICANT: Abartza, Patricia
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
FILE REFERENCE: 469290-55

```

; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-25

Query Match
Best Local Similarity 73.2%; Score 23.4; DB 10; Length 46;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4228 AGCAAAATTAATGTCACGCACTTAAAAA 4268
DB 46 AGCAATACAAATGCAAAAAA 6

RESULT 3
US-09-801-274-957
; Sequence 957, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-957

Query Match
Best Local Similarity 80.6%; Score 22.6; DB 10; Length 31;
Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2453 ACTGCACCAACGACTGATGATGATGAG 2483
DB 1 ACTGCACACACGACGCTGATGATGATCGC 31

RESULT 4
US-09-815-343-1012/c
; Sequence 1012, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1012
```

```

; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-815-343-1012

Query Match
Best Local Similarity 68.9%; Score 22.6; DB 10; Length 50;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4224 AACACACAAATTAATGTCACGCACTTAAAAA 4268
DB 47 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 5
US-09-827-289-21/c
; Sequence 21, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abatzua, Patricia
; APPLICANT: Abatzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-21

Query Match
Best Local Similarity 72.5%; Score 22.4; DB 10; Length 46;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4229 GACCAAAATTAATGTCACGCACTTAAAAA 4268
DB 45 GAGCAATGCAAAATGCAAAAAA 6

RESULT 6
US-09-827-289-22/c
; Sequence 22, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abatzua, Patricia
; APPLICANT: Abatzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-22

Query Match
Best Local Similarity 67.4%; Score 22; DB 10; Length 46;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

	Matches	31,	Conservative	0;	Mismatches	15;	Indels	0;	Gaps	0
QY 4223	TAACAGACAAATTAATGTCACGCACTTA	AAAAAAAAAAAAAAAA	4268	.						
Db 46	TGAGAAATGAAAAAAAAAAAAAAAAAAAA	AAAAA	1							

RESULT 7
US-09-875-519A-13/c
; Sequence 13, Application US/09875519A
; Patent No. US20020068059A1
CURRENT INFORMATION

```

1  APPLICANT: Farries, Timothy C.
2  APPLICANT: Harrison, Richard A.
3  TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
4  FILE REFERENCE: 4-30443/A/IMU/PCT
5  CURRENT APPLICATION NUMBER: US/09/875,519A
6  CURRENT FILING DATE: 2001-06-06
7  PRIOR APPLICATION NUMBER: PCT/GB97/00603
8  PRIOR FILING DATE: 1997-03-04
9  NUMBER OF SEQ ID NOS: 35
10 SOFTWARE: PatentIn Ver. 2.0
11 SEQ ID NO 13
12     LENGTH: 44
13     TYPE: DNA
14 ORGANISM: Homo sapiens
15 US-09-875-519A-13

```

Query Match	0.58;	Score 21.8;	DB 10;	Length 44;
Best Local Similarity	70.78;	Pred. No. 3.4e+04;		
Matches 29; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

Qy 1866 GGTCTCAGAGATGGAGATCATGAAGATGTTGGAAACACA 1906
 ||||| ||| ||||||| ||| ||||| |||
 Db 41 GGTGTGTCATGATGATGATGATGATGTTGGGCCACCCA 1

RESULT 8
US-09-827-289-24/c
; Sequence 24, Application US/09827289
; Patent No. US20020009716A1

```

: TITLE OF INVENTION: Process for Allele Discrimination Using Primer
:
: FILE REFERENCE: 469290-55
:
: CURRENT APPLICATION NUMBER: US/09/827,289
:
: CURRENT FILING DATE: 2001-04-05
:
: PRIOR APPLICATION NUMBER: U.S. 60/194843
:
: PRIOR FILING DATE: 2000-04-05
:
: NUMBER OF SEQ. ID NOS: 35
:
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 24
:
: LENGTH: 46
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
:
: OTHER INFORMATION: use in allele discrimination
:
: US-09-827-289-24

```

Query Match	0.58;	Score 21.8;	DB 10;	Length 46;
Best Local Similarity	70.7%;	Pred. No. 3.4e+04;		
Matches 29; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

QY	4228	AGACAAATTAATGTCACGCACCTTAAAAAAAAAAAAAAAAAAAA	4268
Db	46	AGAGAATAGAAATGATTTTAAAAAAAAAAAAAAAAAAAAAA	6

RESULT 9
US-09-864-785-3604
; Sequence 3604, Application US/09864785

```

; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; ADDITIONAL: Ciba-Geigy Ltd.

```

: TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
 : TITLE OF INVENTION: Levels of NF-Kappa B
 : FILE REFERENCE: 400/022 (MBH000-812-D)
 : CURRENT APPLICATION NUMBER: US/09/864,785
 : CURRENT FILING DATE: 2001-05-23

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3604

```

OTHER INFORMATION:	Description of Artificial Sequence:	Nucleic Acid
US-09-864-785-3604		

Query Match	0.5%	Score 21.8;	DB 9;	Length 48;
Best Local Similarity	60.6%;	Pred. No.	3.5e+04;	
Matches	20;	Conservative	6;	Mismatches 7;
				Indels 0;
				Gaps 0

```

QY 2052 TCCTGAGGAGCAGATGACCTTCAAGGACCTTGGT 2084
      |||:||||| | | ||:|||||| | : |
Db 3 UCCUGAGGAGGAACUCCCUUCAAGGACAUCCU 35

```

RESULT 10
US-09-827-289-26/c
; Sequence 26, Application US/09827289
; Patent No. US20020009716A1

```

? TITLE OF INVENTION: Process for Allele Discrimination Using Primer
? TITLE OF INVENTION: Extension
? FILE REFERENCE: 469290-55
? CURRENT APPLICATION NUMBER: US/09/827,289
? CURRENT FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: U.S. 60/194843
? PRIOR FILING DATE: 2000-04-05
? NUMBER OF SEQ. ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 26
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
? OTHER INFORMATION: use in allele discrimination
? US-09-827-289-26

```

Query Match	0.5%	Score	21.6	DB	10	Length	46
Best Local Similarity	68.2%	Pred. No.	3.8e+04				
Matches	30	Mismatches	14	Indels	0	Gaps	0
	Conservative						

QY	4225	ACAAGACAAATAAATGTCACGCAACTTAAAAA	4268
Db	44	ACGAATAGAAAAA	1

RESULT 11
US-09-827-289-20
; Sequence 20, Application US/09827289
; Patent No. US20020009716A1

: APPLICANT: Abarzuza, Patricia
 : TITLE OF INVENTION: Process for Allele Discrimination using Primer
 : TITLE OF INVENTION: Extension
 : FILE REFERENCE: 469290-55
 : CURRENT APPLICATION NUMBER: US/09/827,289

```
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-20

Query Match
Best Local Similarity 71.8%; Score 21.4; DB 10; Length 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 3386 TTTATAGTTTTTTGTAATTAAGTGCATTCTATGC 3424
Db 5 TTTTATTTTTTTTTTTTTTTTAAATCATTTCTATTTC 43

RESULT 12
US-09-827-289-24
; Sequence 24, Application US/09827289
; Patent No. US2002009716A1
; GENERAL INFORMATION:
; APPLICANT: Abatrua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-24

Query Match
Best Local Similarity 71.8%; Score 21.4; DB 10; Length 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 3386 TTTATAGTTTTTTGTAATTAAGTGCATTCTATGC 3424
Db 5 TTTTATTTTTTTTTTTTTTTTAAATCATTTCTATTTC 43

RESULT 13
US-09-927-777A-72/c
; Sequence 72, Application US/09927777A
; Patent No. US2002017293A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Leisinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-653-A
```

```
; CURRENT APPLICATION NUMBER: US/09/927,777A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/213,906
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/224,631
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/254,392
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/255,235
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 72
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-927-777A-72

Query Match
Best Local Similarity 76.5%; Score 21.2; DB 9; Length 35;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3166 ATATTACAGAGTATTATTTGTAATTCATT 3199
Db 34 ATATGATTAAGATTTTATTTTATTTTATTTT 1

RESULT 14
US-10-023-096-5/c
; Sequence 5, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Golnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:35:24 : Search time 3671 Seconds

(without alignments)
18829.294 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 cccaagaccactctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hlc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hlc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrl:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	26.2	0.6	47	12	BF107886
C 2	25.4	0.6	43	10	AV832677
C 3	24.4	0.6	50	9	AA120437
C 4	24.2	0.6	45	12	BF582680
C 5	24.2	0.6	49	9	AL649742
C 6	24.2	0.6	49	9	AL660945

7	24.2	0.6	49	9	AA545635
C 8	24.2	0.6	50	9	AJ500588
C 9	24.2	0.6	50	17	A2627160
C 10	23.8	0.6	44	9	AU268686
C 11	23.8	0.6	45	9	AL587734
C 12	23.8	0.6	45	12	BF691166
C 13	23.8	0.6	49	12	BF692288
C 14	23.8	0.6	50	9	AU107269
C 15	23.8	0.6	50	9	AU107270
C 16	23.6	0.6	46	2	HSW003158
C 17	23.6	0.6	50	14	BQ393428
C 18	23.4	0.5	49	9	AA116935
C 19	23.2	0.5	49	9	AU267061
C 20	23.2	0.5	49	9	AA590547
C 21	23.2	0.5	49	17	A2587341
C 22	23.2	0.5	50	9	AA853120
C 23	23.2	0.5	47	9	AL627881
C 24	23	0.5	49	2	HSW009339
C 25	23	0.5	49	13	BM183028
C 26	22.8	0.5	45	9	AL795414
C 27	22.8	0.5	45	13	B1330882
C 28	22.8	0.5	50	2	HSW002946
C 29	22.8	0.5	50	9	AJ500405
C 30	22.8	0.5	50	9	AU104655
C 31	22.6	0.5	45	17	A2624922
C 32	22.6	0.5	47	9	AL660275
C 33	22.6	0.5	49	9	AL048743
C 34	22.6	0.5	49	9	AU052653
C 35	22.6	0.5	49	9	AU054068
C 36	22.6	0.5	49	9	BG290798
C 37	22.6	0.5	49	12	BG290798
C 38	22.6	0.5	49	13	B1090256
C 39	22.6	0.5	49	13	B1858831
C 40	22.6	0.5	49	17	A2346760
C 41	22.6	0.5	50	9	AL624136
C 42	22.6	0.5	50	9	AL587874
C 43	22.6	0.5	50	9	AA590944
C 44	22.6	0.5	50	12	BG256941
C 45	22.6	0.5	50	13	B1493940

ALIGNMENTS

RESULT 1
BF107886/c 47 bp mRNA linear EST 19-OCT-2000
LOCUS 601823895R1 NIH_MGC-79 Homo sapiens cDNA clone IMAGE:4043735 3'
DEFINITION
mRNA sequence.
ACCESSION
BF107886
VERSION
BF107886.1 GI:10890412
KEYWORDS
EST.

ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 47)
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT
Email: cga@briemail.nih.gov
Tissue procurement: CLONTECH laboratories, Inc.
CDNA Library Preparation: CLONTECH laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M866 row: n column: 24
High quality sequence start: 8
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

RESULT 4	
BF582680	
LOCUS	45 bp mRNA linear EST 12-DEC-2000
DEFINITION	602094085f1 NCI_GCAP_CO24 Mus musculus cDNA clone IMAGE:4208373 5',
mRNA sequence.	
ACCESSION	BF582680

FEATURES	source
BASE COUNT	43 a 4 c 0 g 2 t
ORIGIN	<pre> 1. 49 /db_xref="taxon:8364" /clone="TGas031111" /clone_1lb="XGC-gastrula" /dev_stage="gastrula (stages 10.5-13 mixed)" /lab_host="Escherichia coli XL1-blue" /note="Vector: PCS107; Site:1: EcoRI; Site:2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from gastrula 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pcs107 with EcoRI at the 5' end and NotI at the 3' end." 0 a 1 c 0 g 48 t </pre>
Query Match	0.6%; Score 24.2; DB 9; Length 49;
Best Local Similarity	71.1%; Pred. No. 1.7e+06;
Matches 32: Conservative	0; Mismatches 13; Indels 0; Gaps 0;
db	4224 AACACGACAAATTAATGTCAACGCACTTAAAAAAAAAAAAAAAA 4268
db	2 AAAAAAAAAAAAAAAAAAACCCCTTAAAAAAAAAAAAAAAAAAAAA 46
RESULT 6	AL660945
LOCUS	AL660945 XGC-neurula Silurana tropicalis cDNA clone TNeu040f06 5',
DEFINITION	mRNA sequence.
ACCESSION	AL660945
VERSION	AL660945.1 GI:17675338
KEYWORDS	EST.
SOURCE	Western clawed frog.
ORGANISM	Silurana tropicalis
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
TITLE	Xenopodinae; Silurana.
JOURNAL	1 (bases 1 to 49)
COMMENT	Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001) Contact: Huckle E Sanger Centre Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SROUNCE.ID: TNeu040f06.sp6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. Location/Qualifiers 1. 49 /organism="Silurana tropicalis" /db_xref="taxon:8364" /clone="TNeu040f06" /clone_1lb="XGC-neurula" /dev_stage="neurula" /lab_host="Escherichia coli DH10B" /note="Vector: PCS107; Site:1: EcoRI; Site:2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pcs107 with EcoRI at the 5' end and NotI at the 3' end."

Plate: 0467 row: L column: 09
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers

FEATURES

1..50

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0467L09"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, p1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321419b1AF12907.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 1 c 1 g 47 t

ORIGIN

Query Match 0.6%; Score 24.2; DB 17; Length 50;
Best Local Similarity 71.1%; Pred. No. 1.7e+06;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4224 AACACGCAAAATGAATGTCAGCAGCTTAATAAAAAAAAAAAAAA 4268

DB 49 AATTAATAAAAAAAAAAAAAA 5

RESULT 10

AU268686

AU268686 44 bp mRNA linear EST 10-MAY-2002
DEFINITION AU268686 VS Dictyostelium discoideum cDNA clone VS1432 3', mRNA
sequence.

ACCESSION AU268686
VERSION AU268686
KEYWORDS GI:20527484

SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

REFERENCE 1 (bases 1 to 44)
Urushihara, H., Morio, T., Saito, T., Koriike, E., Ochiai, H., Maeda, M.,

Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular

stages of Dictyostelium discoideum
Unpublished (2002)

JOURNAL Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

COMMENT

FEATURES

source

1..44
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"

/clone="VS1432"
/clone_lib="VS"
/sex="mat A"
/dev_stage="vegetative"
BASE COUNT 27 a 3 c 1 g 12 t 1 others

Query Match 0.6%; Score 23.8; DB 9; Length 44;
Best Local Similarity 70.5%; Pred. No. 2.1e+06;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4222 TTAAACAGCAAAATGAATGTCAGCAGCTTAATAAAAAAAAAAAAAA 4265

DB 1 TTATCAAAAAAAAAAATGCTGTAATGCTAATATNAAAAAAAAATAA 44

RESULT 11

AL587734/c

AL587734 45 bp mRNA linear EST 02-MAR-2001
LOCUS AL587734 BP Chicken Brain Library gallus gallus cDNA clone
DEFINITION ROS061D09, mRNA sequence.

ACCESSION AL587734
VERSION AL587734.1 GI:13192768
KEYWORDS EST.
SOURCE chicken.

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 45)

REFERENCE Murray, F.
BP Chicken Brain Library
Unpublished (2001)

COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.

FEATURES
source Location/Qualifiers
1..45
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS061D09"
/clone_lib="BP Chicken Brain Library"
/dev_stage="unknown"
/lab_host="Unknown"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GGGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

BASE COUNT 1 a 0 c 10 g 33 t 1 others

Query Match 0.6%; Score 23.8; DB 9; Length 45;
Best Local Similarity 70.5%; Pred. No. 2.1e+06;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4225 ACAAGCAAAATGAATGTCAGCAGCTTAATAAAAAAAAAAAAAA 4268

DB 45 AAAAAAAAAAAAAAAAAACCCCCCNAAAAAAAAAAAAAAAAAAAA 2

RESULT 12

BF691166

BF691166 45 bp mRNA linear EST 22-MAR-2000
LOCUS BF691166
DEFINITION 602247257F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332206 5',

```

ACCESSION      mRNA sequence.
BF691166
VERSION        BF691166.1  GI:11976574
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 45)
AUTHORS        NIH-MGC http://mgc.ncl.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgsabers@mail.nih.gov
                Tissue Procurement: ATCC/DCTD/DTF
                cDNA Library Preparation: CLONETECH Laboratories, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: L1CML198 row b column: 15
                High quality sequence stop: 45.
                Location/Qualifiers
                    1..45
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone_image="433206"
                    /clone_11b="NIH-MGC-62"
                    /l1base_type="melanotic melanoma, high MDR"
                    /lab_host="DH10B (TI phage-resistant)"
                    /note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
                    SfiI (ggcgccgcgcgcgc); Site_2: SfiI (ggccatctatggc);
                    Double-stranded cDNA was prepared from cell line RNA. 5'
                    and 3' adaptors were used in cloning as follows: 5'
                    adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                    sequence: 5'-ATTCAGAGCCGCGCGCCGACATG-dfr(30)BN-3'
                    (where B = A, C, or G and N = A, C, G, or T). Average
                    insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                    contained inserts by PCR. This library was enriched for
                    full-length clones and was constructed by Clontech
                    Laboratories (Palo Alto, Ca)."
BASE COUNT     30 a 7 c 4 g 4 t
ORIGIN
Query Match    0.6% Score 23.8; DB 12; Length 45;
Best Local Similarity 72.1%; Pred. No. 2,1e+06;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4226 CAGGACAAATTAATGTCACGCACTTTAAAAA 4268
DB 2 CAAATACGCAAGACGTCTCTCAAAAAA 44
RESULT 13
LOCUS          BF692288 49 bp mRNA linear EST 22-DEC-2000
DEFINITION     60224917061 NIH-MGC-62 Homo sapiens cDNA clone IMAGE:4334369 5',
                mRNA sequence.
ACCESSION      BF692288
VERSION        BF692288.1  GI:11977696
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 49)
AUTHORS        NIH-MGC http://mgc.ncl.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgsabers@mail.nih.gov
                Tissue Procurement: ATCC/DCTD/DTF

```

```

FEATURES
SOURCE
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4334369"
    /clone_lib="NIH-MGC-62"
    /tissue_type="melanotic melanoma, high MDR"
    /lab_host="DH10B (TI phage-resistant)"
    /note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
    sfiI (ggcgctctggcc); Site_2: sfiI (ggcgctctggcc);
    Double-stranded cDNA was prepared from cell line RNA. 5'
    and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
    sequence: 5'-ATTCTAGAGCGCCGCGCCGATG-dt(30)BN-3'. Average
    insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
    contained inserts by PCR. This library was enriched for
    full-length clones and was constructed by Clontech
    Laboratories (Palo Alto, CA)."
BASE COUNT      31 a      6 c      6 g      6 t
ORIGIN
Query Match      0.6%; Score 23.8; DB 12; Length 49;
Best Local Similarity 72.1%; Pred. No. 2.1e+06;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 4226 CACAGCAAAATTAATGTCACCGCACTTTAAAAA 4268
Db 2 CAATACACGACGACTGTCTCAAAAAAAAAAAAAAAAAA 44
|||||
|||||

RESULT 14
LOCUS AU107269/c 50 bp mRNA Linear EST 30-AUG-2001
DEFINITION AU107269 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNC09312, mRNA sequence.
ACCESSION AU107269
VERSION AU107269
KEYWORDS AU107269.1 GI:13556790
SOURCE EST.
ORGANISM human.
Homo sapiens
Musarivota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mitsuhashi-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LNC09312"
/clone_lib="Sugano Homo sapiens cDNA library"
FEATURES
SOURCE

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:33:52 : Search time 7159 Seconds
(without alignments)
17350.297 Million cell updates/sec

Title: US-09-954-556-3
Perfect score: 4268
Sequence: 1 cccaagaccactcttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rnd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	33	0.8	39	6 AR007163	AR007163 Sequence
C 2	30	0.7	30	6 I32954	I32954 Sequence 15
C 3	30	0.7	30	6 I87104	I87104 Sequence 18
C 4	27.4	0.6	36	9 S41355S1	S41355 BEK-fibrobl
5	27.4	0.6	36	9 S41845S1	S41845 TK25-fibrobl
C 6	25.8	0.6	30	6 A29208	A29208 DNA probe f
C 7	25.8	0.6	30	6 A29211	A29211 Oligonucleo
C 8	25	0.6	25	6 AR090311	AR090311 Sequence
C 9	25	0.6	25	6 AR090312	AR090312 Sequence
10	25	0.6	25	6 AR197346	AR197346 Sequence
C 11	25	0.6	25	6 AR197347	AR197347 Sequence
C 12	24.4	0.6	37	6 AR077808	AR077808 Sequence
13	24.2	0.6	31	6 AX248879	AX248879 Sequence
14	24	0.6	24	6 AR019665	AR019665 Sequence
15	23.6	0.6	42	6 AX347734	AX347734 Sequence
16	23.6	0.6	49	6 AX441065	AX441065 Sequence
C 17	23.6	0.6	50	6 AX159242	AX159242 Sequence
C 18	23.4	0.5	45	6 AX287582	AX287582 Sequence
C 19	23.4	0.5	47	6 AX194754	AX194754 Sequence
20	22.6	0.5	31	6 AX248878	AX248878 Sequence
C 21	22.6	0.5	49	6 AX099434	AX099434 Sequence
C 22	22.6	0.5	50	6 AX261361	AX261361 Sequence
C 23	22.6	0.5	50	6 I36502	I36502 Sequence 1
C 24	22.4	0.5	28	6 AR020621	AR020621 Sequence
C 25	22.4	0.5	46	6 AX287578	AX287578 Sequence
C 26	22	0.5	22	6 AR019666	AR019666 Sequence
C 27	22	0.5	30	6 AR007166	AR007166 Sequence
C 28	22	0.5	45	6 I32116	I32116 Sequence 6
C 29	22	0.5	45	6 I32121	I32121 Sequence 11
C 30	22	0.5	46	6 AX287579	AX287579 Sequence
C 31	22	0.5	50	6 AX164846	AX164846 Sequence
C 32	21.8	0.5	37	6 AB1159	AB1159 Sequence 13
C 33	21.8	0.5	37	6 A98105	A98105 Sequence 19
C 34	21.8	0.5	37	6 A98247	A98247 Sequence 19
C 35	21.8	0.5	37	6 AR205689	AR205689 Sequence
C 36	21.8	0.5	43	6 AR069130	AR069130 Sequence
C 37	21.8	0.5	44	6 A65157	A65157 Sequence 13
C 38	21.8	0.5	44	6 AR038858	AR038858 Sequence
C 39	21.8	0.5	46	6 AX287581	AX287581 Sequence
C 40	21.8	0.5	48	6 AX229262	AX229262 Sequence
C 41	21.6	0.5	46	6 AX287583	AX287583 Sequence
C 42	21.4	0.5	25	6 AR028294	AR028294 Sequence
C 43	21.4	0.5	46	6 AX287577	AX287577 Sequence
C 44	21.4	0.5	46	6 AX287581	AX287581 Sequence
45	21.4	0.5	50	6 AX158618	AX158618 Sequence

ALIGNMENTS

RESULT 1
AR007163/c AR007163 39 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 15 from patent US 5750371.
DEFINITION AR007163
ACCESSION AR007163
VERSION AR007163.1 GI:3966647
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Senoo.M., Watanabe.T. and Igarashi.K.
TITLE Water-soluble mutein of FGF receptor,
JOURNAL Patent: US 5750371-A 15 12-MAY-1998;
FEATURES Location/Qualifiers

```
source 1. .39
BASE COUNT 7 a 11 c 2 g 16 t 3 others
ORIGIN

Query Match 0.8%; Score 33; DB 6; Length 39;
Best Local Similarity 84.6%; Pred. No. 4.6e+03;
Matches 33; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1873 GAGATGAGATGATCAAGATGATTCGGAACACAGAAT 1911
||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 39 GARATGGARATGATGAARATGATCGGGAAGCATAAGAAT 1

RESULT 2 >
LOCUS I32954 132954 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 15 from patent US 5589451.
ACCESSION I32954
VERSION I32954.1 GI:1823745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wilson,S.E.
TITLE Methods and treatments for corneal healing with hepatocyte and
keratinocyte growth factors
JOURNAL Patent: US 5589451-A 15 31-DEC-1996;
FEATURES
source Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 11 a 7 c 4 g 8 t
ORIGIN

Query Match 0.7%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 GATTGAGGTTCTCTATATTCGGAATGTAAC 1271
||||:||||:||||:||||:||||:||||:||||:||||:
Db 30 GATTGAGGTTCTCTATATTCGGAATGTAAC 1

RESULT 3 >
LOCUS I87104 187104 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 18 from patent US 5703047.
ACCESSION I87104
VERSION I87104.1 GI:3206822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wilson,S.E.
TITLE Methods and treatments for corneal healing with growth factors
JOURNAL Patent: US 5703047-A 18 30-DEC-1997;
FEATURES
source Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 11 a 7 c 4 g 8 t
ORIGIN

Query Match 0.7%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 GATTGAGGTTCTCTATATTCGGAATGTAAC 1271
||||:||||:||||:||||:||||:||||:||||:||||:
Db 30 GATTGAGGTTCTCTATATTCGGAATGTAAC 1
```

```
RESULT 4
LOCUS S41355S1 36 bp DNA linear PRI 09-MAY-2000
DEFINITION BEK-fibroblast growth factor receptor [3' region] [human, normal
leukocyte DNA, Genomic, 36 nt, segment 1 of 2].
ACCESSION S41355
VERSION S41355.1 GI:232802
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens normal leukocyte DNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 36)
Champion-Arnaud,P., Ronsin,C., Gilbert,E., Gesnel,M.C.,
Houssaint,E. and Breathnach,R.
TITLE Multiple mRNAs code for proteins related to the BEK fibroblast
growth factor receptor
JOURNAL Oncogene 6 (6), 979-987 (1991)
MEDLINE 91296403
PUBMED 1648704
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 41355] from the original journal article.
This sequence comes from Fig. 4b.
FEATURES
source Location/Qualifiers
1. .36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="leukocyte"
BASE COUNT 13 a 9 c 5 g 9 t
ORIGIN

Query Match 0.6%; Score 27.4; DB 9; Length 36;
Best Local Similarity 96.6%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2549 GAATTCCTCACTCTCACACCAATGAGAA 2577
||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 GAATTCCTCACTCTCACACCAATGAGGTA 29

RESULT 5
LOCUS S41845S1 36 bp DNA linear PRI 09-MAY-2000
DEFINITION TK25-fibroblast growth factor receptor [3' region] [human, normal
leukocyte DNA, Genomic, 36 nt, segment 1 of 2].
ACCESSION S41845
VERSION S41845.1 GI:232806
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens normal leukocyte DNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 36)
Champion-Arnaud,P., Ronsin,C., Gilbert,E., Gesnel,M.C.,
Houssaint,E. and Breathnach,R.
TITLE Multiple mRNAs code for proteins related to the BEK fibroblast
growth factor receptor
JOURNAL Oncogene 6 (6), 979-987 (1991)
MEDLINE 91296403
PUBMED 1648704
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 41845] from the original journal article.
This sequence comes from Fig. 4b.
FEATURES
source Location/Qualifiers
1. .36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="leukocyte"
BASE COUNT 13 a 9 c 5 g 9 t
ORIGIN
```



```

FEATURES
source
    1. .25
    /organism="unknown"
BASE COUNT      3 a      10 c      7 g      5 t
ORIGIN

Query Match          0.6%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 25; Conservative 0; Mismatches 0; Indels

Qy   768  GCTCCATGCTGTGCTCGGCCAAC 792
      |||||||
Db    1    GCTCCATGCTGTGCTCGGCCAAC 25

```

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

BASE COUNT 25 bp DNA linear PAT 20-APR-2002

LOCUS AR197347 25 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 432 from patent US 6352829.

ACCESSION AR197347

VERSION AR197347.1 GI:20247196

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)

AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.

TITLE Methods of assaying differential expression

JOURNAL Patent: US 6352829-A 432 05-MAR-2002;

FEATURES Location/Qualifiers

1..25

/organism="unknown"

BASE COUNT 3 a 7 c 11 g 4 t

ORIGIN

Query Match 0.6%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1179 GCCGCGGGCTGCGCTACCTCAAG 1203

Db 25 GCCGCGGGCTGCGCTACCTCAAG 1

RESULT 12

LOCUS AX077808 37 bp DNA linear PAT 22-FEB-2001

DEFINITION Sequence 9 from Patent WO0107627.

ACCESSION AX077808

VERSION AX077808.1 GI:13157671

KEYWORDS synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 37)

AUTHORS Eisen, A.

TITLE Drosophila recombination-associated protein and methods for use

JOURNAL Patent: WO 0107627-A 9 01-FEB-2001;

ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY (US)

FEATURES Location/Qualifiers

1..37

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="potential mutagenic oligonucleotide"

BASE COUNT 12 a 6 c 11 g 8 t

ORIGIN

Query Match 0.6%; Score 24.4; DB 6; Length 37;

Best Local Similarity 82.4%; Pred. No. 5.8e+05;

Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2133 AAATGTTATTCAGAGATTTAGCAGCCAGAAAT 2166

Db 3 ACAGTGTATTCAGAGATTTGGCAGCCAGGAAT 36

RESULT 13

LOCUS AX248879 31 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 958 from Patent WO0166800.

ACCESSION AX248879

VERSION AX248879.1 GI:15863502

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 31)

AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.

TITLE Human single nucleotide polymorphisms

JOURNAL Patent: WO 0166800-A 958 13-SEP-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES Location/Qualifiers

1..31

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 2 a 13 c 12 g 3 t 1 others

ORIGIN

Query Match 0.6%; Score 24.2; DB 6; Length 31;

Best Local Similarity 83.9%; Pred. No. 6.2e+05;

Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1034 ACCGGCCATCCTCAAGCCGACTGCCGC 1064

Db 1 ACCGGCCATCCTCGCGGGGCTGCCGC 31

RESULT 14

LOCUS AR019665 24 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 4 from patent US 5783683.

ACCESSION AR019665

VERSION AR019665.1 GI:3974779

KEYWORDS Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Morrison, R.S.

TITLE Antisense oligonucleotides which reduce expression of the FGFRI gene

JOURNAL Patent: US 5783683-A 4 21-JUL-1998;

FEATURES Location/Qualifiers

1..24

/organism="unknown"

BASE COUNT 7 a 3 c 8 g 6 t

ORIGIN

Query Match 0.6%; Score 24; DB 6; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.7e+05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 AAGTGTGAGATGGATTAAAGTC 230

Db 1 AAGTGTGAGATGGATTAAAGTC 24

RESULT 15

LOCUS AX347734 42 bp DNA linear PAT 01-FEB-2002

DEFINITION Sequence 84 from Patent WO0196584.

ACCESSION AX347734

VERSION AX347734.1 GI:18495577

KEYWORDS southern root-knot nematode.

ORGANISM Meloidogyne incognita

REFERENCE 1 (bases 1 to 42)

AUTHORS Mushegian, A.R., Taylor, C.G., Feltelson, J.S. and Broshkin, A.M.

TITLE Materials and methods for the control of nematodes

JOURNAL Patent: WO 0196584-A 84 20-DEC-2001;

Akkadix Corporation (US)

FEATURES Location/Qualifiers

1..42

/organism="Meloidogyne incognita"

/db_xref="taxon:6306"

BASE COUNT 18 a 11 c 10 g 3 t

ORIGIN

Query Match 0.6%; Score 23.6; DB 6; Length 42;
Best Local Similarity 76.3%; Pred. No. 9.2e+05;
Matches 29; Conservative 0; Mismatches 9; - Indels 0; Gaps 0;

Oy 1477 AACACGACCAGAAGCGCAGACTTTCAGCAGCGCCGGC 1514
 ||||| |||| | | | | | | | | | |
Db 2 AACACGACGAAGGCGCAACATCAACAGCCTGACGAC 39

Search completed: December 11, 2002, 19:47:34
Job time : 7169 secs

THIS PAGE BLANK (USPTO)

Sequence Alignment

RESERVE 2

LOCUS I32954/C 30 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 15 from patent US 5589451.

ACCESSION I32954

VERSION I32954.1 GI:1823745

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 30)

TITLE Wilson, S.E.

JOURNAL Methods and treatments for corneal healing with hepatocyte and

FEATURES keratinocyte growth factors

Patent: US 5589451-A 15 31-DEC-1996;

Location/Qualifiers

1..30

BASE COUNT 11 a 7 c 4 g 8 t

ORIGIN /organism="unknown"

Query Match 0.7%; Score 30; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.4e+04;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1242 GATTGAGTTCTCTATATTCGGAATGTAC 1271

|||||

Db 30 GATTGAGTTCTCTATATTCGGAATGTAC 1

|||||

RESULT 3

LOCUS I87104/C 30 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 18 from patent US 5703047.

ACCESSION I87104

VERSION I87104.1 GI:3206822

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 30)

TITLE Wilson, S.E.

JOURNAL Methods and treatments for corneal healing with growth factors

FEATURES Patent: US 5703047-A 18 30-DEC-1997;

Location/Qualifiers

1..30

BASE COUNT 11 a 7 c 4 g 8 t

ORIGIN /organism="unknown"

Query Match 0.7%; Score 30; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.4e+04;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1242 GATTGAGTTCTCTATATTCGGAATGTAC 1271

|||||

Db 30 GATTGAGTTCTCTATATTCGGAATGTAC 1

|||||

RESULT 9
 AR090312/c 25 bp DNA 1 linear PAT 07-SEP-2000
 LOCUS AR090312 Sequence 432 from patent US 5994076.
 DEFINITION AR090312
 ACCESSION AR090312
 VERSION AR090312.1 GI:10017067
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Chenchik, A., Jakhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 5994076-A 432 30-NOV-1999;
 FEATURES
 source 1..25
 /organism="unknown"
 BASE COUNT 3 a 7 c 11 g 4 t
 ORIGIN
 Query Match 0.6%; Score 25; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1179 GCCCGACGGGCTGCCCTACCTCAAG 1203
 Db 25 GCCCGACGGGCTGCCCTACCTCAAG 1

7

THIS PAGE BLANK (USPTO)